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OM protein - protein search, using sw model

Run on: July 15, 2003, 08:32:08 ; Search time 70 Seconds
(without alignments)
344.548 Million cell updates/sec

Title:	US-09-937-555A-2
Perfect score:	997

Sequence: 1 EGDYSLCQGREKLDMDMREM.....DYGAGVTCDDDWQNLICIGH 181

Scoring table: BLOSUM62

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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22. /SID5/gcgdata/genseq/genseqp-emb1/AA2001.DAT.*
23. /SID5/gcgdata/genseq/genseqp-emb1/AA2002.DAT.*

Pred. NO. Is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	997	100.0	181	21	AA019333	A hookworm platelet
2	323	32.4	248	20	AAV23611	Neutrophil inhibiti
3	319	32.0	248	20	AAV23605	Canine hookworm ne
4	306.5	30.7	241	20	AAV23610	Canine hookworm ne
5	304.5	30.5	274	20	AAV23604	Canine hookworm ne
6	299	30.0	231	20	AAV23595	Canine hookworm ne
7	298	29.9	231	14	AA052987	Canine hookworm ne
8	296.5	29.7	267	20	AAV23605	Canine hookworm ne
9	286.5	29.7	270	20	AAV23605	Canine hookworm ne
10	280.5	29.1	232	20	AAV23593	Canine hookworm ne

45	15.9	463	21	AAH01373	Neuron-associated
44	15.9	462	20	AAH13352	Amino acid sequenc
43	15.9	461	22	AAH39716	Human polypeptide
42	15.9	460	22	AAH39716	Human polypeptide
41	16.0	459	22	AAH08667	Human FcγR1 poly
40	161.5	458	22	AAH13068	Onchocerca volvu
39	167	457	22	AAH13068	Onchocerca volvu
38	190	456	20	AAH32600	Canine hookworm
37	200	455	20	AAH32600	Canine hookworm
36	200	454	19	AAH32600	Canine hookworm
35	201	453	14	AAH32600	Canine hookworm
34	205	452	13	AAH32600	Canine hookworm
33	214	451	13	AAH32600	Canine hookworm
32	255	450	17	AAH04372	Angiostoma secret
31	255	449	17	AAH04372	Angiostoma secret
30	255	448	12	AAH13070	Angiostoma secret
29	260	447	20	AAH32966	Canine hookworm
28	262	446	20	AAH32966	Canine hookworm
27	265	445	17	AAH04372	Angiostoma secret
26	266	444	17	AAH04372	Angiostoma secret
25	266	443	14	AAH32966	Canine hookworm
24	269	442	20	AAH32600	Canine hookworm
23	284	441	20	AAH32600	Canine hookworm
22	286	440	14	AAH32600	Canine hookworm
21	287	439	27	AAH32600	Canine hookworm
20	290	438	23	AAH20890	Canine hookworm
19	290	437	23	AAH20890	Canine hookworm
18	290	436	23	AAH20890	Canine hookworm
17	290	435	23	AAH20890	Canine hookworm
16	290	434	23	AAH20890	Canine hookworm
15	290	433	20	AAH23592	Canine hookworm
14	290	432	20	AAH23592	Canine hookworm
13	290	431	20	AAH23592	Canine hookworm
12	290	430	20	AAH23592	Canine hookworm
11	290	429	27	AAH23592	Canine hookworm
10	290	428	27	AAH23592	Canine hookworm
9	290	427	27	AAH23592	Canine hookworm
8	290	426	27	AAH23592	Canine hookworm
7	290	425	27	AAH23592	Canine hookworm
6	290	424	27	AAH23592	Canine hookworm
5	290	423	27	AAH23592	Canine hookworm
4	290	422	27	AAH23592	Canine hookworm
3	290	421	27	AAH23592	Canine hookworm
2	290	420	27	AAH23592	Canine hookworm
1	290	419	27	AAH23592	Canine hookworm

ALIGNMENTS

```

RESULT 1
AAB19333
ID      AAB19333  standard; Protein; 181 AA
XX

```

DT 19-FEB-2001 (first entry)
XX
DE A hookworm platelet inhibitor polypeptide.
XX

Ancylostoma caninum.

PD 05-OCT-2000.
yy

PF	30-MAR-2000; 2000WO-US08519.
XX	
PR	31-MAR-1999; 99US-0127239.
VV	

PI Cappello M, Chadderton RC, Del Valle A, Harrison LM,
XX
DR
DR
N-PSDB; AAA75998.
XX

PT Novel platelet inhibitor from hookworms useful for veterinary and

PT medical purposes in cancer therapy, block platelet aggregation by
 PT interfering with binding of cell surface integrin with its respective
 PT ligand
 XX
 PS Claim 1; Page 36; 38pp; English.
 CC The present sequence represents a hookworm platelet inhibitor polypeptide
 CC of *Ancylostoma caninum* rpe hookworm platelet inhibitor not only blocks
 CC platelet aggregation, but also prevents adhesion of platelets to blocks
 CC fibrinogen and possibly also collagen. In vitro, the inhibitor inhibits
 CC b-fibrinogen binding to GPIIb/IIIa. The polypeptides and polynucleotides
 CC are useful for inhibiting platelet function. Thus the polypeptides are
 CC useful for veterinary and medical purposes in vascular biology and cancer
 CC therapy and may also be useful for treating myocardial infarction,
 CC unstable angina, stroke, cerebral and peripheral arterial angioplasty,
 CC thrombocytopenic purpura/hemolytic uremic syndrome, heparin-induced
 CC thrombosis, microvascular and cerebral malaria. They are also useful
 CC for treating variety of cancers by altering the neoplastic state of
 CC tumor cells, repressing gene induction and inhibiting cancer cell
 CC migration on extracellular matrix substances and invasion of distant
 CC tissues. The polypeptides are also useful as vaccines for reducing the
 CC burden of hookworm infections in population at risk.
 CC
 SQ Sequence 181 AA:
 Query Match 100.0%; Score 997; DB 21; Length 181;
 Best Local Similarity 100.0%; Pred. No. 2.1e-95;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 EGDYSLCOOREKLDQDREKFEELHNGYRAAARNYKSKKATMYDCTLEKAYKSAEK 60
 DB 1 EGDYSLCOOREKLDQDREKFEELHNGYRAAARNYKSKKATMYDCTLEKAYKSAEK 60
 OY 61 CSEPESESEENVDFSAATINIPLEAGNSMWEIPELNGKYNKNTNINAMVWDSHD 120
 DB 61 CSEPESESEENVDFSAATINIPLEAGNSMWEIPELNGKYNKNTNINAMVWDSHD 120
 OY 121 KLGCAVAVDSCGTHVCOYGPBKAQKGTIYEGAPGRCSDGAGVTCDDDMQNLGIG 180
 DB 121 KLGCAVAVDSCGTHVCOYGPBKAQKGTIYEGAPGRCSDGAGVTCDDDMQNLGIG 180
 OY 181 H 181
 DB 181 H 181
 OY
 DB
 RESULT 2
 ID AAY23611 standard; Protein: 238 AA.
 XX
 AC AAY23611;
 XX
 DT 03-SEP-1999 (first entry)
 DE Neutrophil inhibitory factor (AcenIF3).
 XX
 KW Neutrophil inhibitory factor; NIF; mutant; shock; stroke;
 KW allograft rejection; vasculitis; autoimmune diabetes; ARDS;
 KW rheumatoid arthritis; inflammatory skin disease; myocardial infarction;
 KW inflammatory bowel disease; adult respiratory distress syndrome;
 KW ischemia-reperfusion injury; acute inflammation; bacterial infection;
 KW vaccine; parasitic worm infection; anti-helminic.
 XX
 AC Ancylostoma ceylanicum.
 OS
 XX
 PN US5919900-A.
 PD 06-JUL-1999.
 XX
 PF 26-MAY-1995; 95US-0450497.
 XX
 PR 23-DEC-1993; 93US-0173510.
 XX
 PR 11-MAY-1992; 92US-0861721.
 PR

PR 24-DEC-1992; 92US-0966972.
 PR 11-MAY-1993; 93US-0060433.
 PR 10-NOV-1993; 93US-0151064.
 PR 26-MAY-1995; 95US-0450497.
 XX
 XX (CORV-) CORVAS INT INC.
 PA
 XX
 PI Foster DL, Moyle M;
 XX
 DR WPI: 1999-403975/34.
 DR N-PSDB; AAK85548.
 XX
 XX
 PT Mutant Neutrophil Inhibitory Factors useful for treating
 PT inflammatory conditions and especially to prevent or decrease
 PT inflammatory responses
 PS
 XX Example 22; Fig 9A-B; 13pp; English.
 CC The specification describes mutant Neutrophil Inhibitory Factors (NIFs),
 CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 137,
 CC or 223 in the wild type sequence (see AAY23591) is replaced by a Gln
 CC residue. NIFs may be useful for treating shock, stroke, acute and
 CC chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid
 CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult
 CC respiratory distress syndrome (ARDS), ischemia-reperfusion injury
 CC following myocardial infarction, and acute inflammation caused by
 CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF
 CC fragments may be used as vaccines against parasitic worm infection.
 CC Anti-NIF antibodies may be useful for detecting infection of a mammalian
 CC host by a parasitic worm, as anti-helminic agents, and in the detection
 CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may
 CC be useful for the detection of NIF mimics or antagonists in other
 CC compounds. Other NIF agonists and inhibitors may also be used as
 CC anti-helminic agents. The present sequence represents a hookworm NIF.
 CC
 SQ Sequence 238 AA:
 Query Match 32.4%; Score 323; DB 20; Length 238;
 Best Local Similarity 36.2%; Pred. No. 3.5e-25;
 Matches 75; Conservative 31; Mismatches 67; Indels 34; Gaps 8;
 OY 1 EGDYSLCOORE-KLDDQDREKFEELHNGYRA-----AFANRKTSMPTM 44
 DB 10 KGDPEPTCKQKNGSMKNELRRLRLHNGYRSLAIGHVNISESENEFTLVAAHSAWRL 69
 OY 45 VYDCTLEKAYKSA-EKCESEPESE---EENVDFSA---TLNIPLEAGNSMWEIPEL 97
 DB 70 DYDDADGSGSYESAIKQCSSMKSSAEDENYVIDNTYEDDEVPALKAISWTSQARNL 129
 OY 98 ----RGKYYKNGKTSNTANAMVWDSHDKLGCAVND--SGKTHVCOYGPBKAQKGTIY 151
 DB 130 THAEEGLPYQMDNSVSDRANVAMDAKELGCAVYTCDDGNTTHVCHGKAAKNTPEIT 189
 OY 152 EGAAPGRCSDGAGVTCDDDMQNLG 178
 DB 190 KVGVPSCNCTETRG-----DEKRVFC 211
 XX
 AC AAY23609;
 XX
 DT 03-SEP-1999 (first entry)
 DE Canine hookworm neutrophil inhibitory factor AcenIF9 polypeptide.
 XX
 KW Neutrophil inhibitory factor; NIF; mutant; shock; stroke;
 KW allograft rejection; vasculitis; autoimmune diabetes; ARDS;
 KW rheumatoid arthritis; inflammatory skin disease; myocardial infarction;
 KW inflammatory bowel disease; adult respiratory distress syndrome;
 KW ischemia-reperfusion injury; acute inflammation; bacterial infection;
 KW

XX AC AAY23610;
 XX DT 03-SEP-1999 (first entry)
 XX DE Canine hookworm neutrophil inhibitory factor AcanNIF18 polypeptide.
 XX KW Neutrophil inhibitory factor; NIF; mutant; shock; stroke;
 XX KW allograft rejection; vasculitis; autoimmune diabetes; ARDS;
 XX KW rheumatoid arthritis; inflammatory skin disease; myocardial infarction;
 XX KW inflammatory bowel disease; adult respiratory distress syndrome;
 XX KW ischemia-reperfusion injury; acute inflammation; bacterial infection;
 XX KW vaccine; parasitic worm infection; antihelminic.
 XX OS Ancylostoma caninum.
 XX PN US5919900-A.
 XX PD 06-JUL-1999.
 XX PF 26-MAY-1995; 9505-0450497.
 XX PR 23-DEC-1993; 9305-0173510.
 XX PR 11-MAY-1992; 9205-0881721.
 XX PR 24-DEC-1992; 9205-0956972.
 XX PR 11-MAY-1993; 9305-0060433.
 XX PR 10-NOV-1993; 9305-0151064.
 XX PR 26-MAY-1995; 9505-0450497.
 XX PA (CONV-) CORVUS INT INC.
 XX PI Foster DL, Moyle M;
 XX DR WPI: 1999-403975/34.
 XX DR N-PSDB: AAX85547.
 XX PT Mutant Neutrophil Inhibitory Factors useful for treating
 XX PT inflammatory conditions and especially to prevent or decrease
 XX PT inflammatory responses
 XX PS Example 21; Fig 16A-V; 131pp; English.
 XX CC The specification describes mutant Neutrophil Inhibitory Factors (NIFs),
 XX CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,
 XX CC or 223 in the wild type sequence (see AY23591) is replaced by a Gln
 XX CC residue. NIFs may be useful for treating shock, stroke, acute and
 XX CC chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid
 XX CC arthritis, inflammatory skin diseases, inflammatory bowel disease,
 XX CC respiratory distress syndrome (ARDS), ischemia-reperfusion injury,
 XX CC following myocardial infarction, and acute inflammation caused by
 XX CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF
 XX CC fragments may be used as vaccines against parasitic worm infection.
 XX CC Anti-NIF antibodies may be useful for detecting infection of a mammalian
 XX CC host by a parasitic worm, as antihelminic agents, and in the detection
 XX CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may
 XX CC be useful for the detection of NIF mimics or antagonists in other
 XX CC compounds. Other NIF agonists and inhibitors may also be used as
 XX CC antihelminic agents. AY23600-10 represent canine hookworm NIF proteins.

QY 88 NSWMSIFEL-----NGKYRNKNGKTSNIANNWVDSHDKLGCAYVDSGK-THVVOYGPPE 142
 Db 126 ISWATFAFNLNKTGCGVYRSIINISFANLAMDTRERVCAYVCKSPRTTHVCHYKRI 185
 QY 143 AKGDGTYIEEGAPCSRCSDGAGVTCDD 172
 Db 186 VEREGKPIYTTGVPCRGCGYANNFCFCHAD 215

RESULT 5
 AAY23604
 ID AAY23604 standard; Protein: 274 AA.
 XX AAY23604:
 AC
 XX
 DT 03-SEP-1999 (first entry)
 XX
 DE Canine hookworm neutrophil inhibitory factor AcanIF4 polypeptide.
 XX
 KW Neutrophil inhibitory factor; NIF; mutant; shock; stroke;
 KW allograft rejection; vasculitis; autoimmune diabetes; ARDS;
 KW rheumatoid arthritis; inflammatory skin disease; myocardial infarction;
 KW inflammatory bowel disease; adult respiratory distress syndrome;
 KW ischemia-reperfusion injury; acute inflammation; bacterial infection;
 KW vaccine; parasitic worm infection; antihelminthic.
 OS Ancylostoma caninum.
 XX
 FN US5919900-A.
 XX
 PD 06-JUL-1999.
 XX
 PF 26-MAY-1995; 95US-0450497.
 XX
 PR 23-DEC-1993; 93US-0173510.
 PR 11-MAY-1992; 92US-0881721.
 PR 24-DEC-1992; 92US-0996972.
 PR 11-MAY-1993; 93US-0060433.
 PR 10-NOV-1993; 93US-0151064.
 PR 26-MAY-1995; 95US-0450497.
 XX
 PA (CORV-) CORVAS INT INC.
 XX
 PI Foster DL, Moyle M;
 XX
 DR WPI: 1999-403975/34.
 DR N-PSDB: AAX85541.
 XX
 PT Mutant Neutrophil Inhibitory Factors useful for treating
 PT inflammatory conditions and especially to prevent or decrease
 PT inflammatory responses
 XX
 PS Example 21; Fig 16A-V; 131pp; English.
 XX
 CC The specification describes mutant Neutrophil Inhibitory Factors (NIFs),
 CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,
 CC or 223 in the wild type sequence (see AAY23591) is replaced by a Gln
 CC residue. NIFs may be useful for treating shock, stroke, acute and
 CC chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid
 CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult
 CC respiratory distress syndrome (ARDS), ischemia-reperfusion injury
 CC following myocardial infarction, and acute inflammation caused by
 CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF
 CC fragments may be used as vaccines against parasitic worm infection.
 CC Anti-NIF antibodies may be used for detecting infection of a mammalian
 CC host by a parasitic worm, as antihelminthic agents, and in the detection
 CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may
 CC be useful for the detection of NIF mimics or antagonists in other
 CC compounds. Other NIF agonists and inhibitors may also be used as
 CC antihelminthic agents. AAY23600-10 represent canine hookworm NIF proteins.
 CC
 XX Sequence 274 AA:

Query Match 30.5%; Score 304.5; Db 20; Length 274;
 Best Local Similarity 32.6%; Pred. No. 3,5e-23;
 Matches 76; Conservative 24; Mismatches 66; Indels 67; Gaps 9;

QY 6 LCOORER-----LDDDRKEMFTELHNGYRAAFARNY----- 36
 Db 20 MCKRRETEMGPFDSNRLOFLAMHNGYRSLAALGHVIGSKOPIDDDYDDYYFYSSYA 79
 QY 37 -RTSKRTMYDCITLDEKAYKSAEK-----SEEPSSEEVADVFSATINI-----PLEGNS 89
 Db 80 PRASKMYLEIDCEDEAKSAYVASNSNISPEGEYDEKRYIFENS-NISEALAKMIS 138
 QY 90 WMSSEIFEL-----RGKYRNKNGKTSNIANNWVDSHDKLGCAYVDC-----SGK 132
 Db 139 WAKEMFNLNKTEEGEGLYRSNHDISNANLAMDTRERFGCAVVCPLGEIDTTSNDDG 198
 QY 133 T-----HYVOYGPPEAKGDKTYIEEGAPCSRCSDYAGV-----TCDD 172
 Db 199 TYANAIHVCHYPRILKEKQIYEVGKPCDRCEYSKANNITSPMNVCMND 251

RESULT 6
 AAY23595
 ID AAY23595 standard; Protein: 231 AA.
 XX AAY23595:
 AC
 XX
 DT 03-SEP-1999 (first entry)
 XX
 DE Canine hookworm neutrophil inhibitory factor isoform clone 3FL.
 XX
 KW Neutrophil inhibitory factor; NIF; mutant; shock; stroke;
 KW allograft rejection; vasculitis; autoimmune diabetes; ARDS;
 KW rheumatoid arthritis; inflammatory skin disease; myocardial infarction;
 KW inflammatory bowel disease; adult respiratory distress syndrome;
 KW ischemia-reperfusion injury; acute inflammation; bacterial infection;
 KW vaccine; parasitic worm infection; antihelminthic.
 OS Ancylostoma caninum.
 XX
 FN US5919900-A.
 XX
 PD 06-JUL-1999.
 XX
 PF 26-MAY-1995; 95US-0450497.
 XX
 PR 23-DEC-1993; 93US-0173510.
 PR 11-MAY-1992; 92US-0881721.
 PR 24-DEC-1992; 92US-0996972.
 PR 11-MAY-1993; 93US-0060433.
 PR 10-NOV-1993; 93US-0151064.
 PR 26-MAY-1995; 95US-0450497.
 XX
 PA (CORV-) CORVAS INT INC.
 XX
 PI Foster DL, Moyle M;
 XX
 DR WPI: 1999-403975/34.
 DR N-PSDB: AAX85541.
 XX
 PT Mutant Neutrophil Inhibitory Factors useful for treating
 PT inflammatory conditions and especially to prevent or decrease
 PT inflammatory responses
 XX
 PS Example 10; Fig 9A-E; 131pp; English.
 XX
 CC The specification describes mutant Neutrophil Inhibitory Factors (NIFs),
 CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,
 CC or 223 in the wild type sequence (see AAY23591) is replaced by a Gln
 CC residue. NIFs may be useful for treating shock, stroke, acute and
 CC chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid
 CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult
 CC respiratory distress syndrome (ARDS), ischemia-reperfusion injury
 CC following myocardial infarction, and acute inflammation caused by

CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF
 CC fragments may be used as vaccines against parasitic worm infection
 CC Anti-NIF antibodies may be useful for detecting infection of a mammalian
 CC host by a parasitic worm, as antihelminthic agents, and in the detection
 CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may
 CC be useful for the detection of NIF mRNAs or antagonists in other
 CC compounds. Other NIF agonists and inhibitors may also be used as
 CC antihelminthic agents. AAY23592-98 represent isoform clones of canine
 CC hookworm NIF.

SO Sequence 231 AA;

Query Match 30.0%; Score 299; DB 20; Length 231;
 Best Local Similarity 35.7%; Pred. No. 1e-22;

Matches 74; Conservative 20; Mismatches 58; Indels 58; Gaps 8;

OY 6 LCOOREK---LDDMRKEMFELANGYRAAFARNY----- 36
 DB 16 ICSQNGTGFGFNDMSRLKFLKLEMHNGYRSLALGHISITEPEESYDDDDGYGEVLAP 75
 OY 37 KTSKMRMYDCTLEEKAYKSAKSCSEPSSE-----EENVDFSAATLNIPLA 86
 DB 76 SASKMRMYEYDCEAKSAKSAKSCSDSSSPGEGYDENKYLLENSNISEARLAI----- 131
 OY 87 GNSWMSSEIFEL---RGKYNNKNGKTSNIANMYWDSHDRLGCAVYDCSGK-----THYV 136
 DB 132 -LSWAKKAFDLNKTGEGVLYRSNLTISNFANLMDTRERFGCAVAKCPLEDTSATTHYV 190
 OY 137 COYGEPAK---DGKTIYEGAPCSRCSY 163
 DB 191 CHY-PKIEGEKEBKQIYKVGTPCGDCSEY 219

RESULT 7

AAR52987 ID AAR52987 standard; Protein: 231 AA.

AC AAR52987;

DT 02-JUN-1994 (first entry)

DE Canine hookworm Neutrophil Inhibitory Factor isoform 2FL.

KW neutrophil inhibitory factor; NIF; glycoprotein; endoparasite;

KW nematode; parasitic worm; canine hookworm; peritoneal inflammation.

OS Ancylostoma caninum.

PN W09323063-A.

PD 25-NOV-1993.

PE 11-MAY-1993; 93MO-US04502.

PR 11-MAY-1992; 92US-0881721.

PR 24-DEC-1992; 92US-0996972.

PA (CORV-) CORVAS INT INC.

PI Foster DL, Moyle M, Vlasuk GP;

PI WPI; 1993-386208/48.

PT New neutrophil inhibitory factor from parasitic worms - for

PT preventing and treating inflammation, also derived nucleic acid,

PS vectors, transformed hosts and antibodies

Example 10; Fig 9; 114pp; English.

CC A canine hookworm cDNA library was screened with a probe amplified

CC using primers 30.2 and 43.3.RC(AA052476 and AA052477, respectively)

CC which were based on sequences of isolated NIF peptide fragments. Seven

CC of the 120 positive clones were isolated for sequence analysis. One

CC isolate, designated clone 1FL, encoded an 825 nucleotide open reading
 CC frame (AA052475). The other clones contained partial ORFs and encoded
 CC partial NIF polypeptides (see AAR52985-R32990) which are thought to
 CC represent six NIF isoforms that are significantly similar to, but
 CC not identical to, the prototypical NIF-1FL polypeptide (AAR42488).

SO Sequence 231 AA;

Query Match 29.9%; Score 298; DB 14; Length 231;
 Best Local Similarity 35.7%; Pred. No. 1.3e-22;

Matches 75; Conservative 20; Mismatches 57; Indels 58; Gaps 9;

OY 6 LCOOREK---LDDMRKEMFELANGYRAAFARNY----- 36
 DB 16 ICSQNGTGFGFNDMSRLKFLKLEMHNGYRSLALGHISITEPEESYDDDDGYGEVLAP 75
 OY 37 KTSKMRMYDCTLEEKAYKSAKSCSEPSSE-----EENVDFSAATLNIPLA 86
 DB 76 SASKMRMYEYDCEAKSAKSAKSCSDSSSPGEGYDENKYLLENSNISEARLAI----- 131
 OY 87 GNSWMSSEIFEL---RGKYNNKNGKTSNIANMYWDSHDRLGCAVYDCSGK-----SGKT-HYV 136
 DB 132 -LSWAKKAFDLNKTGEGVLYRSNLTISNFANLMDTRERFGCAVAKCPLEDTSATTHYV 190
 OY 137 COYGEPAK---DGKTIYEGAPCSRCSY 163
 DB 191 CHY-PKIEGEKEBKQIYKVGTPCGDCSEY 219

RESULT 8

AAY23605 ID AAY23605 standard; Protein: 267 AA.

AC AAY23605;

DT 03-SEP-1999 (first entry)

DE Canine hookworm neutrophil inhibitory factor AcaniNIF6 polypeptide.

KW Neutrophil inhibitory factor; NIF; mutant; shock; stroke;

KW allograft rejection; vasculitis; autoimmune diabetes; ARDS;

KW rheumatoid arthritis; inflammatory skin disease; myocardial infarction;

KW inflammatory bowel disease; adult respiratory distress syndrome;

KW ischemia-reperfusion injury; acute inflammation; bacterial infection;

KW vaccine; parasitic worm infection; antihelminic.

OS Ancylostoma caninum.

PN US5919900-A.

PD 06-JUL-1999.

PE 26-MAY-1995; 95US-0450497.

PR 23-DEC-1993; 93US-0173510.

PR 11-MAY-1992; 92US-0881721.

PR 24-DEC-1992; 92US-0996972.

PR 11-MAY-1993; 93US-0060433.

PR 10-NOV-1993; 93US-0151064.

PR 26-MAY-1995; 95US-0450497.

PA (CORV-) CORVAS INT INC.

PI Foster DL, Moyle M;

PI WPI; 1999-403975/34.

PI N-PSDB; AAK85542.

PT Mutant Neutrophil Inhibitory Factors useful for treating

PT inflammatory conditions and especially to prevent or decrease

Example 21; Fig 16a-V; 131pp; English.

The specification describes mutant Neutrophil Inhibitory Factors (NIFs), where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, or 223 in the wild type sequence (see AAY23591) is replaced by a Gln residue. NIFs may be useful for treating shock, stroke, acute and chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid arthritis, inflammatory skin diseases, inflammatory bowel disease, adult respiratory distress syndrome (ARDS), ischemia-reperfusion injury following myocardial infarction, and acute inflammation caused by bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF fragments may be used as vaccines against parasitic worm infection. Anti-NIF antibodies may be useful for detecting infection of a mammalian host by a parasitic worm, as antihelminthic agents, and in the detection and isolation of NIF from tissue homogenates. Cloned cells etc. NIFs may be useful for the detection of NIF mutants or antagonists in other compounds. Other NIF agonists and inhibitors may also be used as anti-helminic agents. AY23600-10 represent canine hookworm NIF proteins.

Sequence 267 AA:

Query Match 29.7%; Score 296.5; DB 20; Length 267;
Best Local Similarity 34.3%; Pred. No. 2,3e-22;
Matches 72; Conservative 22; Mismatches 63; Indels 53; Gaps 7

QY 6 LCOORERK-----LDDMRKEMTELHNGRYAFAFANY-----KT 38
DB 19 MCCOINETWPGNDIADLOFLAMHNHGYSKALGSLIDSESDDYDYGELPPFPAPSA 78
QY 39 SKRATVWDCTLEEKAKVSKECSEE--PSSEENVDFASNTLT---PLEAGNSWMS 92
DB 79 SKRRYLEYDCERSAVTSSASPDPSPGGYDENKYTFENSN-NISEALKAMISMAK 137
QY 93 EPEEL----RCGVNRKNKGTSINAWMDSHDLGCAYVD-----SGKT 133
DB 138 EAFNLTKTEKVTLQPRIHDISNFALLMREIRFGCAVNCPDELDAIDYEETVATTI 197
QY 134 HVMCGCPGAQGDKGTVEGACARCSDY 163
DB 198 HVYCHPRKINTBEPIIKVGTPCDCEXY 227

RESULT 9
AAI23603
ID AAI23603 standard; Protein; 270 AA.
XX
XX
AC AAY23603;
XX
XX
03-SEP-1999 (first entry)
DE
DE Canine hookworm neutrophil inhibitory factor AcanNIF3 polypeptide.
XX
XX Neutrophil inhibitory factor; NIF; mutant; shock; stroke;
FM allergic rejection; vasculitis; autoimmune diabetes; ARDS;
FM rheumatoid arthritis; inflammatory skin disease; myocardial infarction;
KW inflammatory bowel disease; adult respiratory distress syndrome;
KM ischemia-reperfusion injury; acute inflammation; bacterial infection;
KW vaccine; parasitic worm infection; antihelminc.
XX
OS Ancylotoma caninum.
XX
PD US5919900-A.
FN
FD 06-JUL-1999.
XX
PF 26-MAY-1995; 950S-0450487.
XX
XX 23-DEC-1993; 930S-0173510.
FR 11-MAY-1992; 920S-0861721.
FR 24-DEC-1992; 920S-0936972.
FR 11-MAY-1993; 930S-0060433.
FR 10-NOV-1993; 930S-0151064.
FR 26-MAY-1995; 950S-0450497.
XX
XX

PA (CORV-) CORVAS INT INC.

XX Foster DL, Moyle M;

XX WPI: 1999-403975/34.

DR N-PSDB: AAX85540.

XX

PT Mutant Neutrophil Inhibitory Factors useful for treating

PT Inflammatory conditions and especially to prevent or decrease

PT Inflammatory responses

XX

PS Example 21: Fig 16A-V, 131pp; English.

XX

CC The specification describes mutant Neutrophil Inhibitory Factors (NIFs),

CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,

CC or 223 in the wild type sequence (see AAY23591) is replaced by a Gln

CC residue. NIFs may be useful for treating shock, stroke, acute and

CC chronic allergic rejection, vasculitis, autoimmune diabetes, rheumatoid

CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult

CC respiratory distress syndrome (ARDS), ischemia-reperfusion injury

CC following myocardial infarction, and acute inflammation caused by

CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF

CC fragments may be used as vaccines against parasitic worm infection.

CC Anti-NIF antibodies may be useful for detecting infection of a mammalian

CC host by a parasitic worm, as antihelminthic agents, and in the detection

CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may

CC be useful for the detection of NIF mimics or antagonists in other

CC compounds. Other NIF agonists and inhibitors may also be used as

CC antihelminthic agents. AAY23600-10 represent canine hookworm NIF proteins.

XX

S0 Sequence 270 AA;

Query Match 29.7%; Score 296.5; DB 20; Length 270;

Best Local Similarity 34.3%; Pred. No. 2,3e-22;

Matches 72; Conservative 22; Mismatches 63; Indels 53; Gaps 7;

QY 6 LCQGRK-----LDDMKREFTETLNGRAAFANY-----KT 38

DB 22 MCOQNETEMPGFMDLKLQFLAMNIGRSLAAGHISTIDESDYDYDGLPDRPASA 81

QY 39 SKMRWTYDCTLEEKAYKSAEKCEB---PSEEBNVDYFSAAITLNT---PLEAGSMWS 92

DB 82 SKMRKLETDCEARSAVYTSASCDSSSPGEGYDENKTYFEENSN-NISEAALKAMISMAK 140

QY 93 EIFEL---RGKYYNKGKTSNIAMWYMSHDLGCAVYDC-----SGKT 133

DB 141 EAFNINTEGEGVLYQPNHDISIFNANLMDIREKFGCAVYNGPLGIDADIYDEETAYTI 200

QY 134 HVCQYGPFAKGGKTYIEGAPCSRSDY 163

DB 201 HVCCHYPRINKTEGEPYIVGAPDCDCEY 230

RESULT 10

ID AAY23593 standard; Protein: 232 AA.

AC AAY23593;

XX

XX 03-SEP-1999 (first entry)

DE

DE Canine hookworm neutrophil inhibitory factor isoform clone 3P.

XX

XX Neutrophil inhibitory factor; NIF; mutant; shock; stroke;

XX allergic rejection; vasculitis; autoimmune diabetes; ARDS;

XX rheumatoid arthritis; inflammatory skin disease; myocardial infarction;

XX inflammatory bowel disease; adult respiratory distress syndrome;

XX ischemia-reperfusion injury; acute inflammation; Bacterial infection;

XX vaccine; parasitic worm infection; antihelminthic.

XX

OS *Ancylostoma caninum*.

XX

XX US5919900-A.

```

XX PD 06-JUL-1999.
XX XX
XX PF 26-MAY-1995; 95US-0450497.
XX PR 23-DEC-1993; 93US-0173510.
XX PR 11-MAY-1992; 92US-0881721.
XX PR 24-DEC-1992; 92US-0996972.
XX PR 11-MAY-1993; 93US-0060433.
XX PR 10-NOV-1993; 93US-0151064.
XX PR 26-MAY-1995; 95US-0450497.
XX (CORV-) CORVAS INT INC.
XX Foster DL, Moyle M;
XX WPI; 1999-403975/34.
XX DR
XX PT Mutant Neutrophil Inhibitory Factors useful for treating
XX PT inflammatory conditions and especially to prevent or decrease
XX PT inflammatory responses
XX PS
XX XX Example 10; Fig 9A-E; 131pp; English.
XX CC The specification describes mutant Neutrophil Inhibitory Factors (NIFs),
XX CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,
XX CC or 223 in the wild type sequence (see AAY23591) is replaced by a Glu
XX CC residue. NIFs may be useful for treating shock, stroke, acute and
XX CC chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid
XX CC arthritis, inflammatory skin diseases, ischemia-reperfusion injury
XX CC following myocardial infarction, and acute inflammation caused by
XX CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF
XX CC fragments may be used as vaccines against parasitic worm infection.
XX CC Anti-NIF antibodies may be useful for detecting infection of a mammalian
XX CC host by a parasitic worm, as antihelminthic agents, and in the detection
XX CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may
XX CC be useful for the detection of NIF mimics or antagonists in other
XX CC compounds. Other NIF agonists and inhibitors may also be used as
XX CC antihelminthic agents. AAY23592-98 represent isoform clones of canine
XX CC hookworm NIF.
XX XX
XX SQ Sequence 232 AA;
XX
XX Query Match 29.1%; Score 290.5; DB 20; Length 232;
XX Best Local Similarity 37.3%; Pred. No. 8e-22;
XX Matches 75; Conservative 23; Mismatches 60; Indels 43; Gaps 7;
XX
XX QY 1 EGDYSILCOOREKL---DDMKNEFTELHNGYRAAFARNY-----K 37
XX DB 37 EHDPTCPQNEKMEKGFDDAIRLKTFLAMHNGYSRLAGHSITRESDYDLYDLAYAPR 96
XX QY 38 TSKMRTWVYDCTLEERAKYSAKCSSEPSSE---ENV-----DVPSAATLNIPLDAG 87
XX DB 97 ASKRRYLKDYCEAEKSAVESAKCOTYASSMEKYDENLQVIEDPRDIWHA-----LKA 151
XX QY 88 NSMSEIFEL---RGKYVKNKNGKTSNINANNWDSHDKGCAVYDCSK-THVVCQYGE 142
XX DB 152 ISMATEAFNINKTGEGVYRSITLIDISNFAMLADTREKYGCAVVCSPRTTHVVCYPRK 211
XX QY 143 AKGDKRTIEGAPGRCSDY 163
XX DB 212 SRRENPIYTTGNRCGGS DY 232
XX
XX RESULT 11
XX ID AAE20891
XX XX AAE20891 standard; Protein; 257 AA.
XX AC AAE20891;
XX XX
XX DT 01-JUL-2002 (first entry)
XX XX

```

```

DE DB Ancylostoma caninum mature neutrophil inhibitory factor (NIF) 1 protein.
XX XX
XX KW Neutrophil inhibitory factor; NIF; therapy; inflammatory condition;
XX KW abnormal neutrophil activation; shock; stroke; allograft rejection;
XX KW vasculitis; autoimmune diabetes; rheumatoid arthritis; head trauma;
XX KW inflammatory skin disease; inflammatory bowel disease; antibacterial;
XX KW adult respiratory distress syndrome; ARDS; ischemia-reperfusion injury;
XX KW myocardial infarction; bacterial infection; sepsis; cerebroprotective;
XX KW bacterial meningitis; immunosuppressive; antiparasitic; antihelminthic;
XX KW vaccine; antinflammatory; vasotropic.
XX XX
XX OS Ancylostoma caninum.
XX XX
XX PN W0200216584-A2.
XX XX
XX PD 28-FEB-2002.
XX XX
XX PE 15-AUG-2001; 2001MO-US25733.
XX PR 23-AUG-2000; 2000US-0644942.
XX PR 28-FEB-2001; 2001US-0797410.
XX PA (PFIZ ) PRIZER PROD INC.
XX PA (CORV-) CORVAS INT INC.
XX PI Pluschke SB, Geldart RW, Ho L, Koehler MA, Okedadi CA, Plas SJ,
XX PI Zhu MM, Hawrylyk SJ, Moyle M;
XX XX WPI; 2002-292063/33.
XX XX
XX PT Preparing Neutrophil Inhibitory Factor for treating shock, by growing
XX PT cell line expressing the factor in animal component-free medium such as
XX PT inoculum growth medium, production growth medium or nutrient feed
XX PS Claim 42; Page 92-94; 100pp; English.
XX XX
XX CC The invention relates to a method for the preparation of neutrophil
XX CC inhibitory factor (NIF) comprising growing a cell line expressing NIF
XX CC in an animal component-free medium selected from inoculum growth medium,
XX CC a production growth medium and a nutrient feed to give a production
XX CC culture. The method is useful for preparation of NIF. Animal component-
XX CC free production growth medium is useful for preparation of recombinant
XX CC proteins. NIF is useful for preventing or treating inflammatory
XX CC conditions characterised by abnormal neutrophil activation, for treating
XX CC shock, stroke, acute and chronic allograft rejection, vasculitis,
XX CC autoimmune diabetes, rheumatoid arthritis, head trauma, inflammatory
XX CC skin diseases, inflammatory bowel disease, adult respiratory distress
XX CC syndrome (ARDS), ischemia-reperfusion injury following myocardial
XX CC infarction and acute inflammation caused by bacterial infection, such as
XX CC sepsis or bacterial meningitis. NIF is also useful as diagnostic agents,
XX CC to screen other compounds to detect NIF mimics or to detect NIF
XX CC antagonists for their ability to affect NIF binding to the CD11b/CD18
XX CC receptor, as a vaccine against parasitic worm infections in mammals, and
XX CC for prophylaxis and therapy of parasitic infections. The present sequence
XX CC is Ancylostoma caninum mature NIF1 protein.
XX XX
XX SQ Sequence 257 AA;
XX
XX Query Match 29.1%; Score 290; DB 23; Length 257;
XX Best Local Similarity 34.3%; Pred. No. 1e-21;
XX Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;
XX
XX QY 14 DDMKNEFTELHNGYRAAFARNY-----KTSKMTWVYDCTL 50
XX DB 18 NDSIRLOFLAMHNGYRSKTLGHISTESESDDDDDFGLPFAFARASKRRYLEYDCEA 77
XX QY 51 EERAYKSAKCSSE---PSSEENVDSAAATLNI---PLEANSWSEIFEL-----R 98
XX DB 78 EKSAYVASARNCSDSSPPREGYDENKTYFENSN-NISDAKAMISNAEAKNLKRTKEG 136
XX QY 99 GRKYVKNKNGKTSNINANNWDSHDKGCAVYDC-----SGKT-----HYVCQYGE 142
XX

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Db	137	GVLTRSHDHSINFAIMLAMDREKFGCAVYVNCPLGEIDDETFNHDEGTATTIHVHCYPKI	196
Oy	143	AKGDKTIVEEGAPSCSDY 163 :: :: ::	
Db	197	NRTGGPIYKVGTPCDDCEX 217	
RESULT 12			
ID	AA123606	standard; Protein: 272 AA.	
AC	AA123606;		
DC	03-SEP-1999	(first entry)	
DE	Canine hookworm neutrophil inhibitory factor AcanNIF7 polypeptide.		
KM	Neutrophil inhibitory factor; NIF; mutant; shock; stroke; allergic rejection; vasculitis; autoimmune diabetes; ARDS; Rheumatoid arthritis; inflammatory skin disease; myocardial infarction; inflammatory bowel disease; adult respiratory distress syndrome; ischemia-reperfusion injury; acute inflammation; bacterial infection; vaccine; parasitic worm infection; antihelminic.		
OS	Ancylostoma caninum.		
XX	US5919900-A.		
XX	06-JUL-1999.		
PF	26-MAY-1995;	95US-0450497.	
PR	23-DEC-1993;	93US-0173510.	
PR	11-MAY-1992;	92US-0881721.	
PR	24-DEC-1992;	92US-0996972.	
PR	11-MAY-1993;	93US-0060433.	
PR	10-NOV-1993;	93US-0151064.	
PR	26-MAY-1995;	95US-0450497.	
XX	(CORV-) CORVAS INT INC.		
PA	Foster DL, Moyle M;		
PJ	WPI; 1999-403975/34.		
DR	N-PADB: AMX85543.		
XX			
PT	Mutant Neutrophil Inhibitory Factors useful for treating		
PT	inflammatory conditions and especially to prevent or decrease		
PT	inflammatory responses		
PS	Example 21: Flg 16A-V; 131pp; English.		
CC	The specification describes mutant Neutrophil Inhibitory Factors (NIFs) where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, or 223 in the wild type sequence (see AA123591) is replaced by a Gln residue. NIFs may be useful for treating shock, stroke, acute and chronic allergic rejection, vasculitis, autoimmune diabetes, rheumatoid arthritis, inflammatory skin diseases, inflammatory bowel disease, adult respiratory distress syndrome (ARDS), ischemia-reperfusion injury following myocardial infarction, and acute inflammation caused by bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF fragments may be used as vaccines against parasitic worm infection. Anti-NIF antibodies may be useful for detecting infection of a mammalian host by a parasitic worm, as antihelminic agents, and in the detection and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may be useful for the detection of NIF mutants or antagonists in other compounds. Other NIF agonists and inhibitors may also be used as antihelminic agents. AA123600-10 represent canine hookworm NIF proteins.		
XX	Sequence	272 AA;	
Query Match	29.1%;	Score 290;	DB 20; Length 272;
Best Local Similarity	34.3%;	Pred. No. 1.le-21;	

```

Matches      69;  Conservative      23;  Mismatches      57;  Indels      52;  Gaps      7

Oy      14 DDDRMCFEELHNGYRAAFARNY-----KTSKMTWVYDCTL 50
Db      33 NDSIRLQFLAHNGYRSKTLALGHISTEESDDDDDFGLPDPAPRAKMYLEYDCEA 92
Oy      51 EEKAYVSAKSGSEE---PSEEEYDVFAAATLNT---PLEAGSNMMSIFEL-----R 98
Db      93 EKSAYVSAKNSCSDSSSPGECYDENEYIFENSN-NISEAALAKMISNAKAFVLNKTDEG 151
Oy      99 GKRYNNKGTSTNINAWMYSHDKLGCVYDC-----SKT-----HYVCGTGP 142
Db      152 GVLRSNHDISFENLMLADREKECAVNCPLGEIDETHIDEGYATTHTYCHIFKPI 211
Oy      143 AKGDGKTYIEGAPCSRCSYD 163
Db      212 NKEGGPIIKVGTPTCDXCSEY 232

RESULT 13
AAR42488
AAR42488 standard; Protein; 274 AA.
AAR42488;
AAR42488;
02-JUN-1994 (first entry)
Canine hookworm Neutrophil Inhibitory Factor 1FL.
Xc      DE      Canine hookworm Neutrophil Inhibitory Factor 1FL.
Xc      KM      neutrophil inhibitory factor; NIF, glycoprotein; endoparasite;
Xc      KM      nematode; parasitic worm; canine hookworm, peritoneal inflammation.
Xc      OS      Ancylostoma caninum.
Xc      PN      MO9323063-A.
Xc      PD      25-NOV-1993.
Xc      PF      11-MAY-1993; 93WO-US04502.
Xc      PF      11-MAY-1992; 92US-0881721.
Xc      PR      24-DEC-1992; 92US-0996972.
Xc      PR      (CONV-) CORVAS INT INC.
Xc      PA      Foster DL, Moyle M, Vlausk GP;
Xc      PI      MPI; 1993-386208/48.
Xc      DR      N-PSDB; AA052475.
Xc      XX      New neutrophil inhibitory factor from parasitic worms - for
Xc      PT      preventing and treating inflammation, also derived nucleic acid,
Xc      PT      vectors, transformed hosts and antibodies
Xc      PS      Claim 23; Fig 8; 114pp; English.
Xc      XX      A canine hookworm cDNA library was screened with a probe amplified
Xc      CC      using primers 30.2 and 43.3 (AA052476 and AA052477, respectively) which
Xc      CC      were based on sequences of isolated NIF peptide fragments. Seven of
Xc      CC      the 120 positive clones were isolated for sequence analysis. One
Xc      CC      isolate, designated clone 1FL, encoded an 825 nucleotide open reading
Xc      CC      frame (AA052475). The other clones contained partial ORFs and encoded
Xc      CC      partial NIF polypeptides (see AA852985-R52990) which are thought to
Xc      CC      represent six NIF isoforms that are significantly similar to, but
Xc      CC      not identical to, the prototypical NIF-1FL polypeptide (AAR42488).
Xc      CC      Sequence      274 AA.

Query Match      29.1%; Score 290; DB 14; Length 274;
Best Local Similarity 34.3%; Pred.No. 1.1e-21;
Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7.

14 DDDRMCFEELHNGYRAAFARNY-----KTSKMTWVYDCTL 50

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```
DB      35 NDSIRLOFLAMHNGYNSKLAIGHISITESESDDDDDGFLPDPAPRASKMYLEIDCEA 94
QY      51 EERAYSAKNCSE--PSEENVDFSAATLNI---PLEAGNSWSEIPEL-----R 98
DB      95 EKSAVMSARNCSDSSPEGYDENKTYIFENS-NISEAALAKMISAKAEFLNLTKEGE 153
QY      99 GKYVNRKGTSTNANWYDSDHDKLCAVYDC-----SGKT-----HYVCGRPE 142
DB      154 GVLVRSNHDISNFANLMDAREKFCGAVNCPGLGEIDETNHDGYATYTIHVCHYPRKI 213
QY      143 AKDGRKTYIEGAPCSRCSY 163
DB      214 NRTGQPIYKVGTPCDDCSEY 234

RESULT 14
AA23600
ID      AA23600 standard; Protein: 274 AA.
XX
AC      AA23600;
XX
DT      03-SEP-1999 (first entry)
XX
DE      Canine hookworm neutrophil inhibitory factor NIF-1FL polypeptide.
XX
KM      Neutrophil inhibitory factor; NIF; mutant; shock; stroke;
KM      allograft rejection; vasculitis; autoimmune diabetes; ARDS;
KM      rheumatoid arthritis; inflammatory skin disease; myocardial infarction;
KM      inflammatory bowel disease; adult respiratory distress syndrome;
KM      ischemia-reperfusion injury; acute inflammation; bacterial infection;
KM      vaccine; parasitic worm infection; antihelminic.
XX
OS      Ancylostoma caninum.
XX
PN      US5919900-A.
XX
PD      06-JUL-1999.
XX
PF      26-MAY-1995; 95US-0450497.
XX
PR      23-DEC-1993; 93US-0173510.
PR      11-MAY-1992; 92US-0881721.
PR      24-DEC-1992; 92US-0996972.
PR      11-MAY-1993; 93US-0060433.
PR      10-NOV-1993; 93US-0151064.
PR      26-MAY-1995; 95US-0450497.
XX
PA      (CORV-) CORVAS INT INC.
XX
PI      Foster DL, Moyle M;
XX
DR      WPI; 1999-403975/34.
XX
DR      N-PSDB; AAX85537.
XX
KT      Mutant Neutrophil Inhibitory Factors useful for treating
KT      inflammatory conditions and especially to prevent or decrease
KT      inflammatory responses
XX
Example 21; Fig 16A-V; 131pp; English.
XX
CC      The specification describes mutant Neutrophil Inhibitory Factors (NIFs),
CC      where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,
CC      or 233 in the wild type sequence (see AA23591) is replaced by a Glu
CC      residue. NIFs may be useful for treating shock, stroke, acute and
CC      chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid
CC      arthritis, inflammatory skin diseases, inflammatory bowel disease, adult
CC      respiratory distress syndrome (ARDS), ischemia-reperfusion injury
CC      following myocardial infarction, and acute inflammation caused by
CC      bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF
CC      fragments may be used as vaccines against parasitic worm infection.
CC      Anti-NIF antibodies may be useful for detecting infection of a mammalian
CC      host by a parasitic worm, as antihelminic agents, and in the detection
```

```
CC      and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may
CC      be useful for the detection of NIF mimics or antagonists in other
CC      compounds. Other NIF agonists and inhibitors may also be used as
CC      antihelminic agents. AA23600-10 represent canine hookworm NIF proteins.
XX
SO      Sequence 274 AA;
XX
Query Match 29.1%; Score 290; DB 20; Length 274;
Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;
DB      14 DDDMRKMTTELHNGYNAFAFRNY-----KTSKRTVYDCTL 50
DB      35 NDSIRLOFLAMHNGYNSKLAIGHISITESESDDDDDGFLPDPAPRASKMYLEIDCEA 94
QY      51 EERAYSAKNCSE--PSEENVDFSAATLNI---PLEAGNSWSEIPEL-----R 98
DB      95 EKSAVMSARNCSDSSPEGYDENKTYIFENS-NISEAALAKMISAKAEFLNLTKEGE 153
QY      99 GKYVNRKGTSTNANWYDSDHDKLCAVYDC-----SGKT-----HYVCGRPE 142
DB      154 GVLVRSNHDISNFANLMDAREKFCGAVNCPGLGEIDETNHDGYATYTIHVCHYPRKI 213
QY      143 AKDGRKTYIEGAPCSRCSY 163
DB      214 NRTGQPIYKVGTPCDDCSEY 234

RESULT 15
AA23601
ID      AA23601 standard; Protein: 274 AA.
XX
AC      AA23601;
XX
DT      03-SEP-1999 (first entry)
XX
DE      Canine hookworm neutrophil inhibitory factor PCR-NIF polypeptide.
XX
KM      Neutrophil inhibitory factor; NIF; mutant; shock; stroke;
KM      allograft rejection; vasculitis; autoimmune diabetes; ARDS;
KM      rheumatoid arthritis; inflammatory skin disease; myocardial infarction;
KM      inflammatory bowel disease; adult respiratory distress syndrome;
KM      ischemia-reperfusion injury; acute inflammation; bacterial infection;
KM      vaccine; parasitic worm infection; antihelminic.
XX
OS      Ancylostoma caninum.
XX
PN      US5919900-A.
XX
PD      06-JUL-1999.
XX
PF      26-MAY-1995; 95US-0450497.
XX
PR      23-DEC-1993; 93US-0173510.
PR      11-MAY-1992; 92US-0881721.
PR      24-DEC-1992; 92US-0996972.
PR      11-MAY-1993; 93US-0060433.
PR      10-NOV-1993; 93US-0151064.
PR      26-MAY-1995; 95US-0450497.
XX
PA      (CORV-) CORVAS INT INC.
XX
PI      Foster DL, Moyle M;
XX
DR      WPI; 1999-403975/34.
XX
DR      N-PSDB; AAX85538.
XX
KT      Mutant Neutrophil Inhibitory Factors useful for treating
KT      inflammatory conditions and especially to prevent or decrease
KT      inflammatory responses
XX
Example 21; Fig 16A-V; 131pp; English.
XX
```

The specification describes mutant Neutrophil Inhibitory Factors (NIFs), where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, or 223 in the wild type sequence (see AAY23591) is replaced by a Glu residue. NIFs may be useful for treating shock, stroke, acute and chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid arthritis, inflammatory skin diseases, inflammatory bowel disease, adult respiratory distress syndrome (ARDS), ischemia-reperfusion injury following myocardial infarction, and acute inflammation caused by bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF fragments may be used as vaccines against parasitic worm infection. Anti-NIF antibodies may be useful for detecting infection of a mammalian host by a parasitic worm, as antihelminthic agents, and in the detection and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may be useful for the detection of NIF mimics or antagonists in other compounds. Other NIF agonists and inhibitors may also be used as antihelminthic agents. AAY23591-10 represent canine hookworm NIF proteins.

Sequence 274 AA:

Query Match 29.1%; Score 290; DB 20; Length 274;
Best Local Similarity 33.8%; Pred. No. 1.1e-21;
Matches 72; Conservative 25; Mismatches 60; Indels 56; Gaps 9;

QY 6 LCQGR---EKIDDKREFTELNGYRAFAFANY-----KT 38
DB 23 MCOQNGTEMDFNDSTRLOFLMANGYRSKALGHISTEESDDDDFGFLDPAPRA 82
QY 39 SKMRTMYDCTLEKAYKSAKCSSE---PSEEEYDVFSATLNT---PLEAGNSMWS 92
DB 83 SMRTLEYDEAEKSAVMSARNCSDSSPPGEGYDENKTYFENSN-NISEALKAMISMAK 141
QY 93 EYFEL---RGK---VYNKNGKTSNIANNVMDSHDKLGCAYVDC-----SGRT-- 133
DB 142 EAFNINKTKEGEVELYRSNHDISNFANLAMDAKREKFCAYVNCPLGEIDETIHDEGTVA 201
QY 134 ---HYVCOYGEAKGDKTIYEGAPCSRCSY 163
DB 202 TTIHVCHYPRINKTEGEPIYKVGTPDCDCEY 234

RESULT 16
AAY23592
ID AAY23592 standard; Protein; 274 AA.

XX AAY23592;
AC
XX
DT 03-SEP-1999 (first entry)
XX
DE Canine hookworm neutrophil inhibitory factor isoform clone 1FL.
XX
KM Neutrophil inhibitory factor; NIF; mutant; shock; stroke;
KM allograft rejection; vasculitis; autoimmune diabetes; ARDS;
KM rheumatoid arthritis; inflammatory skin disease; myocardial infarction;
KM inflammatory bowel disease; adult respiratory distress syndrome;
KM ischemia-reperfusion injury; acute inflammation; bacterial infection;
KM vaccine; parasitic worm infection; antihelminthic.
XX
OS Ancylostoma caninum.
XX
PN US5919900-A.
XX
PD 06-JUL-1999.
XX
PE 26-MAY-1995; 95US-0450497.
XX
XX 23-DEC-1993; 93US-0173510.
PR 11-MAY-1992; 92US-0881721.
PR 24-DEC-1992; 92US-0996972.
PR 11-MAY-1993; 93US-0060433.
PR 10-NOV-1993; 93US-0151064.
PR 26-MAY-1995; 95US-0450497.
XX
PA (CORV-) CORVAS INT. INC.

XX
PI Poster DL, Moyle M;
XX
DB WPI: 1999-403975/34.
XX
PT Mutant Neutrophil inhibitory factors useful for treating
PT inflammatory conditions and especially to prevent or decrease
PT inflammatory responses
XX
XX Example 10; Fig 9A-E; 131pp; English.

The specification describes mutant Neutrophil Inhibitory Factors (NIFs), where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, or 223 in the wild type sequence (see AAY23591) is replaced by a Glu residue. NIFs may be useful for treating shock, stroke, acute and chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid arthritis, inflammatory skin diseases, inflammatory bowel disease, adult respiratory distress syndrome (ARDS), ischemia-reperfusion injury following myocardial infarction, and acute inflammation caused by bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF fragments may be used as vaccines against parasitic worm infection. Anti-NIF antibodies may be useful for detecting infection of a mammalian host by a parasitic worm, as antihelminthic agents, and in the detection and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may be useful for the detection of NIF mimics or antagonists in other compounds. Other NIF agonists and inhibitors may also be used as antihelminthic agents. AAY23592-98 represent isoform clones of canine hookworm NIF.

Sequence 274 AA:

Query Match 29.1%; Score 290; DB 20; Length 274;
Best Local Similarity 34.3%; Pred. No. 1.1e-21;
Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;

QY 14 DDDRMREFTELNGYRAFAFANY-----KTSKMTMYDCTL 50
DB 35 NDSIRLOFLMANGYRSKALGHISTEESDDDDFGFLDPAPRAKMYLEYDCEA 94
QY 51 EKAYKSAKCSSE---PSEEEYDVFSATLNT---PLEAGNSMWSYFEL-----R 98
DB 95 EKAYVMSARNCSDSSPPGEGYDENKTYFENSN-NISEALKAMISMAKFAFNLNTRKEGE 153
QY 99 GKYTNKNGKTSNIANNVMDSHDKLGCAYVDC-----SGRT---HYVCOYGE 142
DB 154 GVLRSNHDISNFANLAMDAKREKFCAYVNCPLGEIDETIHDEGTVAATTIHYVCHYKFI 213
QY 143 AKGDGKTIYEGAPCSRCSY 163
DB 214 NKTGOPYTKVGTGTPDCDCEY 234

RESULT 17
AAY23591
ID AAY23591 standard; Protein; 274 AA.

XX AAY23591;
AC
XX
DT 03-SEP-1999 (first entry)
XX
DE Neutrophil inhibitory factor clone 1FL.
XX
KM Neutrophil inhibitory factor; NIF; mutant; shock; stroke;
KM allograft rejection; vasculitis; autoimmune diabetes; ARDS;
KM rheumatoid arthritis; inflammatory skin disease; myocardial infarction;
KM inflammatory bowel disease; adult respiratory distress syndrome;
KM ischemia-reperfusion injury; acute inflammation; bacterial infection;
KM vaccine; parasitic worm infection; antihelminthic.
XX
OS Ancylostoma caninum.
XX
PN US5919900-A.

PD 06-JUL-1999. 95US-0450497.
 XX 26-MAY-1995;
 XX 23-DEC-1993; 93US-0173510.
 PR 11-MAY-1992; 92US-0881721.
 PR 24-DEC-1992; 92US-0996972.
 PR 11-MAY-1993; 93US-0060433.
 PR 10-NOV-1993; 93US-0151064.
 PR 26-MAY-1995; 95US-0450497.
 XX (CORV-) CORVAS INT INC.
 XX Foster DL, Moyle M;
 XX WPI: 1999-403975/34.
 DR N-PSDB; AAK85535.
 XX
 XX Mutant Neutrophil Inhibitory Factors useful for treating
 PT inflammatory conditions and especially to prevent or decrease
 PT inflammatory responses
 PS Claim 1; Fig 8A-E; 131pp; English.
 XX The specification describes mutant Neutrophil Inhibitory Factors (NIFs),
 CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,
 CC or 223 in the wild type sequence (see AAY3591) is replaced by a Gln
 CC residue. NIFs may be useful for treating shock, stroke, acute and
 CC chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid
 CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult
 CC respiratory distress syndrome (ARDS), ischemia-reperfusion injury
 CC following myocardial infarction, and acute inflammation caused by NIF
 CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF
 CC fragments may be used as vaccines against parasitic infection of a mammalian
 CC host by a parasitic worm, as anti-infective agents, and in the detection
 CC and isolation of NIF from tissue homogenates of cloned cells etc. NIFs may
 CC be useful for the detection of NIFs or NIFs or antagonists in other
 CC compounds. Other NIF agonists and inhibitors may also be used as
 CC anti-infective agents. The present sequence represents a canine hookworm
 CC NIF.
 XX Sequence 274 AA;
 XX 50
 Query Match 29.1%; Score 290; DB 20; Length 274;
 Best Local Similarity 34.3%; Pred. No. 1.1e-21;
 Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;
 QY 14 DDDMEFTELHNGYRAAFARNY-----KTSKMTWYDCTL 50
 DB 35 NDSINLOFLAMHNGYRSKALGHISTESESDDDDDFGLPDPFAPRAKMYLEYDCEA 94
 QY 51 EEKAVKSAEKSEB--PSSEENVVFSATLNI--PLEAGNSWMSSEIFEL-----R 98
 DB 95 EKSAYMSARNCSDSSSPPEGYDENKFIENSN-NISEAALKAMISWAKENFNLKTEGE 153
 QY 99 GKYNNKNGKTSNINAMWMDSHDKLGCAVYDC-----SGKT-----HVVCQYGE 142
 DB 154 GYLXRNDHDSIFNANLMDAREKFGCAVYVNCPLGEIDETNHDGETYATTIHVCHYKPI 213
 QY 143 AKGDGTYEEGAPCSRCSDY 163
 DB 214 NKEGQPIYKVGTPDDCSEY 234
 RESULT 18
 AAU97699
 ID AAU97699 standard; Protein: 274 AA.
 AC AAU97699;
 XX
 XX 13-AUG-2002 (first entry)
 XX

DE Canine hookworm Neutrophil Inhibitory Factor (NIF) protein sequence.
 XX
 XX Canine hookworm; dog hookworm; neutrophil inhibitory factor; NIF;
 KW pathophysiological condition; neutrophilic; thrombolytic; stroke;
 KW fibrinolytic; ischemic damage; reperfusion injury; head injury;
 KW post-ischemic reperfusion injury; post-ischemic cerebral inflammation;
 KW reperfusion-reperfusion injury; myocardial infarction; anti-inflammatory;
 KW cardiac; synergist.
 XX Ancylostoma caninum.
 XX
 XX Key Location/Qualifiers
 XX Peptide 1-17
 XX Protein 18-274
 XX /label= Mature canine hookworm NIF protein
 XX /note= "Specifically claimed in claim 2"
 XX W020032446-A2.
 XX 25-APR-2002.
 XX 15-OCT-2001; 2001MO-IB01936.
 XX 17-OCT-2000; 2000GB-0025473.
 XX (PRIZ) PRIZER LTD.
 XX (PRIZ) PRIZER INC.
 XX Breasley CJ, Butler P, Chaiwala SB, Chopp M, Krams M, Looby M;
 XX Macintyre F, McElroy AB, McHarg AD;
 XX WPI: 2002-452373/48.
 XX N-PSDB; AAK52544.
 XX Use of a combination of at least one Neutrophil Inhibitory Factor and
 PT at least one other neuroprotective or thrombolytic/fibrinolytic agent
 PT for treating e.g. stroke, traumatic head injury or post-ischemic
 PT cerebral inflammation
 PS Claim 2; Fig 2; 110pp; English.
 XX The present invention relates to a new method for treating
 CC pathophysiological conditions involving neutrophils. The method of the
 CC invention involves administering to a subject, simultaneously/separately/
 CC sequentially Neutrophil Inhibitory Factor (NIF) and another
 CC neuroprotective or thrombolytic/fibrinolytic agent in amounts that render
 CC the combination of the 2 or more agents effective in treating
 CC pathophysiological conditions involving neutrophils. The combination of
 CC at least one Neutrophil Inhibitory Factor (NIF) and at least one other
 CC neuroprotective or thrombolytic/fibrinolytic agent for the treatment of
 CC pathophysiological conditions involving neutrophils is ischemic damage
 CC and/or reperfusion injury e.g. stroke, traumatic head injury,
 CC post-ischemic reperfusion injury, post-ischemic cerebral inflammation
 CC or reperfusion-reperfusion injury following myocardial infarction.
 CC The present amino acid sequence represents the canine (dog) hookworm
 CC Neutrophil Inhibitory Factor (NIF) protein of the invention.
 XX
 XX Sequence 274 AA;
 XX 50
 Query Match 29.1%; Score 290; DB 23; Length 274;
 Best Local Similarity 34.3%; Pred. No. 1.1e-21;
 Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;
 QY 14 DDDMEFTELHNGYRAAFARNY-----KTSKMTWYDCTL 50
 DB 35 NDSINLOFLAMHNGYRSKALGHISTESESDDDDDFGLPDPFAPRAKMYLEYDCEA 94
 QY 51 EEKAVKSAEKSEB--PSSEENVVFSATLNI--PLEAGNSWMSSEIFEL-----R 98
 DB 154 GYLXRNDHDSIFNANLMDAREKFGCAVYVNCPLGEIDETNHDGETYATTIHVCHYKPI 213
 QY 143 AKGDGTYEEGAPCSRCSDY 163
 DB 214 NKEGQPIYKVGTPDDCSEY 234

DB 95 EKSAVNSARNCSSSPREGYDENKXIFENSN-NISEAALKAMISRAKFAFNKTRKEE 153
QY 99 GRYNKNKGTNSINAMWVDSHDKLGCAVDC-----SGKT-----HYVCOYGE 142
DB 154 GVLVRSNHDISNFAINLMDAREKFCGAVVNCPLGEIDDETNDHGETVATTIHVCHPKI 213
QY 143 AKGDGKTIIEGAPCSRCSY 163
DB 214 NKTGQPIYKVGTFPCDDCSEY 234

RESULT 19
AAE20890
ID AAE20890 standard; Protein: 274 AA.
XX
AC AAE20890;
XX
DT 01-JUL-2002 (first entry)
XX
DE PEE14/NIF1c insert DNA encoded Ancylostoma caninum NIF1 protein.
XX
KW Neutrophil inhibitory factor; NIF; therapy; inflammatory condition;
KW abnormal neutrophil activation; shock; stroke; allograft rejection;
KW vasculitis; autoimmune diabetes; rheumatoid arthritis; head trauma;
KW inflammatory skin disease; inflammatory bowel disease; antibacterial;
KW adult respiratory distress syndrome; ARDS; ischaemia-reperfusion injury;
KW myocardial infarction; bacterial infection; sepsis; cerebroprotective;
KW bacterial meningitis; immunosuppressive; antiparasitic; antihelminthic;
KW vaccine; antiinflammatory; vasotropic.
XX
OS Ancylostoma caninum.
XX
FH Key
FT Location/Qualifiers
FT 1..17
FT /label= Signal_peptide
FT 18..274
FT /label= Mature_NIF1_protein
FT 18..26
FT /note= "N-terminal region"
FT 36..50
FT /note= "D-85 peptide"
FT 77..90
FT /note= "D-67 peptide"
FT 88..96
FT /note= "D-13 peptide"
FT 116..125
FT /note= "D-53, D54 peptides"
FT 116..145
FT /note= "D-102 peptide"
FT 134..141
FT /note= "D-20 peptide"
FT 135..141
FT /note= "K-34a peptide"
FT 142..172
FT /note= "K-50a peptide"
FT 162..172
FT /note= "D-96 peptide"
FT 177..189
FT /note= "K-46b peptide"
FT 224..236
FT /note= "T-15-6 peptide"
FT 251..261
FT /note= "D-61 peptide"
FT 267..274
FT /note= "K-48, T-22-10 peptides"
XX
PN WO200216584-A2.
XX
PD 28-FEB-2002.
XX
PF 15-AUG-2001; 2001MO-US25733.
XX
PR 23-AUG-2000; 2000US-0644942.

PR 28-FEB-2001; 2001US-0797410.
XX
PA (PRIZ) PRIER PROD INC.
PA (CORV-) CORVAS INT INC.
XX
PI Plusckell SB, Geldart RM, Ho L, Koehler MA, Okediedl CA, Plas SJ;
PI Zhu KM, Hawrylik SJ, Moyle M;
XX
DR WPI: 2002-292063/33.
XX
N-PSDB: AAD33306.
XX
PT Preparing Neutrophil Inhibitory Factor for treating shock, by growing
PT cell line expressing the factor in animal component-free medium such as
PT inoculum growth medium, production growth medium or nutrient feed
XX
PS Example 1; Fig 1; 100pp; English.
XX
CC The invention relates to a method for the preparation of neutrophil
CC inhibitory factor (NIF) comprising growing a cell line expressing NIF
CC in an animal component-free medium selected from inoculum growth medium,
CC a production growth medium and a nutrient feed to give a production
CC culture. The method is useful for preparation of NIF. Animal component-
CC free production growth medium is useful for preparation of recombinant
CC proteins. NIF is useful for preventing or treating inflammatory
CC conditions characterised by abnormal neutrophil activation, for treating
CC shock, stroke, acute and chronic allograft rejection, vasculitis,
CC autoimmune diabetes, rheumatoid arthritis, head trauma, inflammatory
CC skin diseases, ischaemia-reperfusion injury following myocardial
CC infarction, in which neutrophil infiltration and activation has been
CC implicated and acute inflammation caused by bacterial infection, such as
CC sepsis or bacterial meningitis. NIF is also useful as diagnostic agents,
CC to screen other compounds to detect NIF mimics or to detect NIF
CC receptors, as a vaccine against parasitic worm infections in mammals, and
CC for prophylaxis and therapy of parasitic infections. The present sequence
CC is Ancylostoma caninum NIF1 protein encoded by PEE14/NIF1c insert DNA.
XX
SQ Sequence 274 AA:
XX
Query Match 29.18; Score 290; DB 23; Length 274;
Best Local Similarity 34.38; Pred. No. 1,1e-21;
Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;
QY 14 DDDKREMTLHNGIRGAFAKNT-----KTSKMTAVYDCTL 50
DB 35 NDSIRLQFLAHNNGIRSKLALGHISTESESDDDDGFLPDPAPRAKMYLEYDEA 94
QY 51 EERKYSAEKCSSE--PSSEENVDVESAAATLN---PLEAGNSWMSIFEL-----R 98
DB 95 EKSAVNSARNCSSSPREGYDENKXIFENS-NISEAALKAMISRAKFAFNKTRKEE 153
QY 99 GRYNKNKGTNSINAMWVDSHDKLGCAVDC-----SGKT-----HYVCOYGE 142
DB 154 GVLVRSNHDISNFAINLMDAREKFCGAVVNCPLGEIDDETNDHGETVATTIHVCHPKI 213
QY 143 AKGDGKTIIEGAPCSRCSY 163
DB 214 NKTGQPIYKVGTFPCDDCSEY 234

RESULT 20
AAV23599
ID AAV23599 standard; Protein: 289 AA.
XX
AC AAV23599;
XX
DT 03-SEP-1999 (first entry)
XX
DE Protein encoded by two-clstron Met-NIF expression cassette.
XX
KW Neutrophil inhibitory factor; NIF; mutant; shock; stroke;
KW allograft rejection; vasculitis; autoimmune diabetes; ARDS;


```

KM Rheumatoid arthritis; inflammatory skin disease; myocardial infection;
KM Inflammatory bowel disease; adult respiratory distress syndrome;
KM Ischemia-reperfusion injury; acute inflammation; bacterial infection;
KM vaccine; parasitic worm infection; antihelminic.
XX Synthetic.
OS Ancyclostoma caninum.
PN US9519900-A.
PD 06-JUL-1999.
PP 26-MAY-1995; 95US-0450497.
PR 23-DEC-1993; 93US-0173510.
PR 11-MAY-1992; 92US-0881721.
PR 14-DEC-1992; 92US-0996972.
PR 11-MAY-1993; 93US-0060433.
PR 10-NOV-1993; 93US-0151064.
PR 26-MAY-1995; 95US-0450497.
PA (CORV-) CORVAS INT INC.
PI Foster DL, Moyle M;
PT MPI: 1999-403975/34.
DR N-PSDB; AAX85536.
XX XX
XX Mutant Neutrophil Inhibitory Factors useful for treating
XX inflammatory conditions and especially to prevent or decrease
XX inflammatory responses
XX Example 20; Fig 15A-D; 11pp; English.
XX CC The specification describes mutant Neutrophil Inhibitory Factors (NIFs)
CC where at least 1 of the Asp residues at positions 19, 87, 110, 130, 197,
CC or 223 in the wild type sequence (see AY23591) is replaced by a Glp
CC residue. NIFs may be useful for treating shock, stroke, acute and
CC chronic allograft rejection, vasculitis, autoimmune bowel disease, rheumatoid
CC arthritis, inflammatory skin diseases, ischemia-reperfusion injury
CC following myocardial infarction, and acute inflammation caused by
CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF
CC fragments may be used as vaccines against parasitic worm infection.
CC Anti-NIF antibodies may be useful for detecting infection of a mammalian
CC host by a parasitic worm, as anthelmintic agents, and in the detection
CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may
CC be useful for the detection of NIF mimics or antagonists in other
CC compounds. Other NIF agonists and inhibitors may also be used as
CC antihelminic agents. The present sequence is encoded by a two-cliston
CC Met-NIF expression cassette of Pms-NI1/3.
SS Sequence 289 AA:
SQ
Query Match          29.1%; Score 290; DB 20; Length 289;
Best Local Similarity 34.3%; Pred NO 1,2e-21;
Matches   69; Conservative 23; Mismatches 57; Indels 52; Gaps 7
Oy      14 DDDREMEFELINGRAAFARN-----KTSKRMTAVYDCTL 50
Db      50 NDSTRQFLAMNGRSLMLGHISTSESDDDDFGFLDPFAFRSKRRFLDECA 105
Oy      51 EERKYSAKRCGE---PSEEENDVFSAATLTI---PLEAGNSWSEIFEL-----R 98
Db      110 EKSYAKSARCKDSSPPEGIDENKTITENSNIISEPALKAMISMAEAPFNKTKIGE 166
Oy      99 GKTYNNKGSTSIANMWWDSHDKLCGAAYDC-----SGKT-----HYVCQYPE 142
Db      169 GVLRSHDHISNFALMDAREKEFGAVVNCPLQEIDEFTHNDGETVAATIIVHCHYPKI 228
Oy      143 AKGDGTIIIEGAPCSQCDY 163
Db      229 NKTEGPITYKVETPDDCCEY 249
```

RESULT 21
 ID AA23607
 ID AA23607 standard; Protein; 274 AA.
 AC AAC
 XX AA23607;
 DT 03-SEP-1999 (first entry)
 XX
 XX Canine hookworm neutrophil inhibitory factor Acanif9 polypeptide.
 DE
 KW Neutrophil inhibitory factor; NIF; mutant; shock; stroke;
 KW allograft rejection; vasculitis; autoimmune diabetes; ARDS;
 KW rheumatoid arthritis; inflammatory skin disease; myocardial infarction;
 KW inflammatory bowel disease; adult respiratory distress syndrome;
 KW ischemia-reperfusion injury; acute inflammation; bacterial infection;
 KW vaccine; parasitic worm infection; antihelminic.
 OS Ancylostoma caninum.
 PN US9119900-A.
 PD 06-JUL-1999
 PF 26-MAY-1995; 950S-0450497.
 PR 23-DEC-1993; 930S-0173510.
 PR 11-MAY-1993; 930S-0881721.
 PR 24-DIC-1993; 930S-0936972.
 PR 11-MAY-1993; 930S-0060433.
 PR 10-NOV-1993; 930S-0151064.
 PR 26-MAY-1995; 950S-0450497.
 PA (CORV-) CORVAS INT INC.
 PI Foster DL, Moyle M;
 DR NPI: 1999-403975/34.
 DR N-PSDB; AAX85344.
 PT Mutant Neutrophil Inhibitory Factors useful for treating
 PI inflammatory conditions and especially to prevent or decrease
 PI inflammatory responses
 XX Example 21; Fig 16A-V; 13pp; English.
 XX
 XX The specification describes mutant Neutrophil Inhibitory Factors (NIFs),
 CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,
 CC or 223 in the wild type sequence (see AAY3591) is replaced by a Gln
 CC residue. NIFs may be useful for treating shock, stroke, acute and
 CC chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid
 CC arthritis, inflammatory skin diseases, vasculitis, autoimmune diabetes, adult
 CC respiratory distress syndrome (ARDS), ischemia-reperfusion injury
 CC following myocardial infarction, and acute inflammation caused by
 CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF
 CC fragments may be used as vaccines against parasitic worm infection.
 CC Anti-NIF antibodies may be useful for detecting infection of a mammalian
 CC host by a parasitic worm, as antihelminthic agents, and in the detection
 CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may
 CC be useful for the detection of NIF mimics or antagonists in other
 CC compounds. Other NIF agonists and inhibitors may also be used as
 CC antihelminthic agents. AAY23600-10 represent canine hookworm NIF proteins.
 XX
 XX Sequence 274 AA:
 14 DDDRENTTELTNNGYRAAFARNY-----KTSKRRTVVCCCL 50
 Query Match 28.8%; Score 287; DB 20; Length 274;
 Best Local Similarity 34.3%; Pied. No. 2,je-21;
 Matches 69; Conservative 22; Mismatches 58; Indels 52; Gaps 7

```

QY 51 BEAKYKSNKSEKSEF---PSSEBENDVPSAATLNI---PLENGNSWSEIPEL-----R 98
DB 95 EBSAHSNRKCSOSSSPGEGIDENKTYITENSN-NISEBALKAMISMAEAKNLKTEBEG 153
QY 99 GKVYKNGKTSNIANNWDSHDKLCAVYDC-----SGKT-----HYVCOYGP 142
DB 154 GVLKRSNHDISNFPANLAMDAREKFCAYVNCPLGEIDETIHGETVATTHVCHYKPI 213
QY 143 AKGDGKTYEGAPCSRCSY 163
DB 214 NKEGQPTKYEVTGTPCDDCSGY 234

RESULT 22
AAR52985 standard; Protein; 234 AA.
AAR52985;
AAR52985;
02-JUN-1994 (first entry)
Canine hookworm Neutrophil Inhibitory Factor isoform 3P.
neutrophil inhibitory factor; NIF; glycoprotein; endoparasite;
nematode; parasitic worm; canine hookworm; peritoneal inflammation.
Ancylostoma caninum.
MO9323063-A.
25-NOV-1993.
11-MAY-1993; 93MO-US04502.
11-MAY-1993; 92US-0881721.
24-DEC-1992; 92US-0996972.
(CORV-) CORVAS INT INC.
Foster DL, Moyle M, Vlasak GP;
WPI; 1993-386208/48.
New neutrophil inhibitory factor from parasitic worms - for
preventing and treating inflammation, also derived nucleic acid,
vectors, transformed hosts and antibodies
Example 10; Fig 9; 114p; English.
A canine hookworm cDNA library was screened with a probe amplified
using primers 30.2 and 43.3.RC(AA052476 and AA052477, respectively)
which were based on sequences of isolated NIF peptide fragments. Seven
of the 120 positive clones were isolated for sequence analysis. One
clone, designated clone 1FL, encoded an 825 nucleotide open reading
frame (AA052475). The other clones contained partial ORFs and encoded
partial NIF polypeptides (see AAR52985-R52990) which are thought to
represent six NIF isoforms that are significantly similar to, but
not identical to, the prototypical NIF-1FL polypeptide (AAR42488).
Sequence 234 AA;
Query Match 28.7%; Score 286.5; DB 14; Length 234;
Best Local Similarity 36.9%; Pred. No. 2.1e-21;
Matches 75; Conservative 22; Mismatches 61; Indels 45; Gaps 7;
QY 1 EDDYSLCOOREKL-----DDDMEMETELAHNGYRAAFARRY----- 36
DB 37 EDDPFCPONGEKMEKGFDAIRLAKFLAMHNGYSRALGHVSTESDYLDLDLIXAP 96
QY 37 KTSKRMWYDCLLEKAKRSKESPEPSEE---ENV-----DVFSAAITNIPLEA 86
DB 97 RASNAKTIKIDCAEASAKSATESAKCOTTASWEXIDENQVIEDPKDINMAA-----LKA 151

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QY 87 GNSWSEIPEL-----RGKYKNGKTSNIANNWDSHDKLCAVYDCS--GKTHVCOYG 140
DB 152 IISMWAEANLNLKKGEGVYRSILDISNFPANLAMDAREKFCAYVNCSPRTTHVCHYKPI 211
QY 141 PEAKGDGKTYEGAPCSRCSY 163
DB 212 KKSRRRENPIYTTGNRCGCSY 234

RESULT 23
AA23608 standard; Protein; 270 AA.
AA23608;
AA23608;
03-SEP-1999 (first entry)
Canine hookworm neutrophil inhibitory factor AcanNIF24 polypeptide.
Neutrophil Inhibitory Factor; NIF; mutant; shock; stroke;
allergic rejection; vasculitis; autoimmune diabetes; ARDS;
rheumatoid arthritis; inflammatory skin disease; myocardial infarction;
inflammatory bowel disease; adult respiratory distress syndrome;
ischemia-reperfusion injury; acute inflammation; bacterial infection;
vaccine; parasitic worm infection; antihelminic.
Ancylostoma caninum.
US919900-A.
06-JUL-1999.
26-MAY-1995; 95US-0450497.
23-DEC-1993; 93US-0173510.
11-MAY-1992; 92US-0881721.
24-DEC-1992; 92US-0996972.
11-MAY-1993; 93US-0060433.
10-NOV-1993; 93US-0151064.
26-MAY-1995; 95US-0450497.
(CORV-) CORVAS INT INC.
Foster DL, Moyle M;
WPI; 1999-403975/34.
N-PSDB; AAX85545.
Mutant Neutrophil Inhibitory Factors useful for treating
inflammatory conditions and especially to prevent or decrease
inflammatory responses
Example 21; Fig 16A-V; 131p; English.
The specification describes mutant Neutrophil Inhibitory Factors (NIFs),
where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,
or 223 in the wild type sequence (see AA23591) is replaced by a Gln
residue. NIFs may be useful for treating shock, stroke, acute and
chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid
arthritis, inflammatory skin diseases, inflammatory bowel disease, adult
respiratory distress syndrome (ARDS), ischemia-reperfusion injury
following myocardial infarction, and acute inflammation caused by
bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF
fragments may be used as vaccines against parasitic worm infection.
Anti-NIF antibodies may be useful for detecting infection of a mammalian
host by a parasitic worm, as antihelminic agents, and in the detection
and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may
be useful for the detection of NIF mimics or antagonists in other
antihelminic agents. AA23600-10 represent canine hookworm NIF proteins.
Sequence 270 AA;

```

Query Match	28.5%	Score 284.5	DB 20	Length 270
Best Local Similarity	43.8%	Prod No 4.1e-21		
Matches 69	Conservative	22	Mismatches 58	Indels 55
				Gaps 7

QY	14	DDDMREMFELHNGCAAFARNT-----	-----KTSKRTAVYD	47
DB	35	NDRIKQFLAMHNGRSLALGHSITDSESESDDDEYDVPATYAPATASKRRTLEYD	94	
QY	48	CTLEEAAYSARKSESE---PSEEENDVPSAATLNI---PLAEGNSWMSBIFEL----	97	
DB	95	CEAEKSAIYMSANCSDDSSPPEGYDKNKIFENSN-NISEAALKAMISAKAEAFNLKTE	153	
QY	98	--RGKYRNKNGKTSNINAMWDSHDLGCAVVC-----SGKT-----HVCQY	139	
DB	154	EGCGVLYRSNHDINFPANLAMDREKFGCAVVCPLGEIDGTTIDGERTVATTHVCH	213	
QY	140	GPEAKGDGKTYIEGACGSCSDY	163	
DB	214	PKMKTEGEPIYKVKKPCRCDSSEY	237	

RESULT 24	
AAV23602	
ID	AAV23602 standard; Protein; 263 AA.
AC	AAV23602;
DF	03-SEP-1999 (first entry)
DE	Canine hookworm neutrophil inhibitory factor PCR-NIF20 polypeptide.
XX	
KV	Neutrophil inhibitory factor; NIF; mutant; shock; stroke;
KV	allergic rejection; vasculitis; autoimmune diabetes; ARDS;
KV	rheumatoid arthritis; inflammatory skin disease; myocardial infarction;
KV	inflammatory bowel disease; adult respiratory distress syndrome;
KV	ischemia-reperfusion injury; acute inflammation; bacterial infection;
KV	vaccine; parasitic worm infection; antihelminic.
XX	
OS	Ancylostoma caninum.
XX	
PN	US95919900-A.
XX	
PD	06-JUL-1999.
XX	
PF	26-MAY-1995; 95US-0450497.
XX	
PR	23-DEC-1993; 93US-0173510.
PR	11-MAY-1992; 92US-0881721.
PR	24-DEC-1992; 92US-0996872.
PR	11-MAY-1993; 93US-0060433.
PR	10-NOV-1993; 93US-0151064.
PR	26-MAY-1995; 95US-0450497.
XX	
PA	(CORV-) CORVAS INT INC.
PI	Poster DL, Moyle W;
DR	WPI, 1999-403975/34.
XX	
DR	N-PSDB; AAX85539.
PT	Mutant Neutrophil Inhibitory Factors useful for treating
PT	inflammatory conditions and especially to prevent or decrease
PT	inflammatory responses
XX	
PS	Example 21; Fig 16A-V; 131pp; English.
XX	
CC	The specification describes mutant Neutrophil Inhibitory Factors (NIFs)
CC	where at least 1 of the Asp residues at positions 18, 87, 110, 130, 137,
CC	or 223 in the wild type sequence (see AAV23591) is replaced by a Gln
CC	residue. NIFs may be useful for treating shock, stroke, acute and
CC	chronic allergic rejection, vasculitis, autoimmune diabetes, rheumatoid
CC	arthritis, inflammatory skin diseases, inflammatory bowel disease, adult

[illegible]

CC of the 120 positive clones were isolated for sequence analysis. One
 CC isolate, designated clone 1FL, encoded an 825 nucleotide open reading
 CC frame (AA032475). The other clones contained partial ORFs and encoded
 CC partial NIF polypeptides (see AA032985-R52990) which are thought to
 CC represent six NIF isoforms that are significantly similar to, but
 CC not identical to, the prototypical NIF-1FL polypeptide (AA032488).

XX Sequence 224 AA;

Query Match 26.7%; Score 266; DB 14; Length 224;
 Best Local Similarity 33.8%; Pred. No. 2.7e-19;

Matches 66; Conservative 21; Mismatches 56; Indels 52; Gaps 7;

QY 14 DDDMRMFTLHNGYRAAFARNT-----KTSKRTMYDCT 49

DB 31 NDSIRLOFLAMHNGYSKIALGHISITDESESDDEYDYWAPAPAPASAKRILEYDCE 90

QY 50 LEEKAYSAKCE--EPSSSEENVDFSAATLNT---PLEAGSNWSEIFEL-----R 98

DB 91 AEKSHMSARNCSDSSSPEDENKTYIFENSN-NISEBALAKAMISMAKFAFNLKTEEGE 149

QY 99 GAVYNNKGTSTNIANWVDSHDKLCAVYDC-----SGKT-----HYVCOYGP 142

DB 150 GVLIRSNHDISNFAFLAMDTRERKFCGAVVNCPLGEIDGTTIHDEGYATTIHVCHYPM 209

QY 143 AKGDGTYIEGAPC 157

DB 210 NKTEGOPYIKVKPC 224

RESULT 26

AA032596

ID AA032596 standard; Protein; 224 AA.

XX AA032596;

DT 03-SEP-1999 (first entry)

DE Canine hookworm neutrophil inhibitory factor isoform clone 4FL.

XX Neutrophil inhibitory factor; NIF; mutant; shock; stroke;

XX allograft rejection; vasculitis; autoimmune diabetes; ARDS;

KM rheumatoid arthritis; inflammatory skin disease; myocardial infarction;

KM inflammatory bowel disease; adult respiratory distress syndrome;

KM ischemia-reperfusion injury; acute inflammation; bacterial infection;

KM vaccine; parasitic worm infection; anthelmintic.

XX Ancylostoma caninum.

XX US5919900-A.

XX 06-JUL-1999.

XX 26-MAY-1995; 95US-0450497.

XX 23-DEC-1993; 93US-0173510.

XX 11-MAY-1993; 92US-0881721.

XX 24-DEC-1993; 92US-0986972.

XX 11-MAY-1993; 93US-0060433.

XX 10-NOV-1993; 93US-0151064.

XX 26-MAY-1995; 95US-0450497.

XX (CORV-) CORVAS INT INC.

XX Foster DL, Moyle M;

XX WPI; 1999-403975/34.

XX Mutant Neutrophil Inhibitory Factors useful for treating

XX inflammatory conditions and especially to prevent or decrease

XX inflammatory responses

XX Example 10; Fig 9A-E; 131pp; English.

XX

CC The specification describes mutant Neutrophil Inhibitory Factors (NIFs),

CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,

CC or 223 in the wild type sequence (see AA032591) is replaced by a Glu

CC residue. NIFs may be useful for treating shock, stroke, acute and

CC chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid

CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult

CC respiratory distress syndrome (ARDS), ischemia-reperfusion injury

CC following myocardial infarction, and acute inflammation caused by

CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF

CC fragments may be used as vaccines against parasitic worm infection

CC and NIF antibodies may be useful for detecting infection of a mammalian

CC host by a parasitic worm, as anthelmintic agents, and in the detection

CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may

CC be useful for the detection of NIF mimics or antagonists in other

CC compounds. Other NIF agonists and inhibitors may also be used as

CC anthelmintic agents. AA032592-96 represent isoform clones of canine

CC hookworm NIF.

XX Sequence 224 AA;

QY 14 DDDMRMFTLHNGYRAAFARNT-----KTSKRTMYDCT 49

DB 31 NDSIRLOFLAMHNGYSKIALGHISITDESESDDEYDYWAPAPAPASAKRILEYDCE 90

QY 50 LEEKAYSAKCE--EPSSSEENVDFSAATLNT---PLEAGSNWSEIFEL-----R 98

DB 91 AEKSHMSARNCSDSSSPEDENKTYIFENSN-NISEBALAKAMISMAKFAFNLKTEEGE 149

QY 99 GAVYNNKGTSTNIANWVDSHDKLCAVYDC-----SGKT-----HYVCOYGP 142

DB 150 GVLIRSNHDISNFAFLAMDTRERKFCGAVVNCPLGEIDGTTIHDEGYATTIHVCHYPM 209

QY 143 AKGDGTYIEGAPC 157

DB 210 NKTEGOPYIKVKPC 224

XX Ancylostoma caninum.

XX US5919900-A.

XX 06-JUL-1999.

XX 26-MAY-1995; 95US-0450497.

XX 23-DEC-1993; 93US-0173510.

XX 11-MAY-1993; 92US-0881721.

XX 24-DEC-1993; 92US-0986972.

XX 11-MAY-1993; 93US-0060433.

XX 10-NOV-1993; 93US-0151064.

XX 26-MAY-1995; 95US-0450497.

XX (CORV-) CORVAS INT INC.

XX Foster DL, Moyle M;

XX WPI; 1999-403975/34.

XX Mutant Neutrophil Inhibitory Factors useful for treating

XX inflammatory conditions and especially to prevent or decrease

XX inflammatory responses

XX Example 10; Fig 9A-E; 131pp; English.

XX Example 10; Fig 9A-E; 131pp; English.

XX Example 10; Fig 9A-E; 131pp; English.

XX Example 10; Fig 9A-E; 131pp; English.

XX Example 10; Fig 9A-E; 131pp; English.

XX Example 10; Fig 9A-E; 131pp; English.

XX Example 10; Fig 9A-E; 131pp; English.

XX Example 10; Fig 9A-E; 131pp; English.

XX Example 10; Fig 9A-E; 131pp; English.

XX Example 10; Fig 9A-E; 131pp; English.

XX Example 10; Fig 9A-E; 131pp; English.

XX Example 10; Fig 9A-E; 131pp; English.

XX Example 10; Fig 9A-E; 131pp; English.

XX Example 10; Fig 9A-E; 131pp; English.

XX Example 10; Fig 9A-E; 131pp; English.

XX WPI; 1996-477130/47.
DR N-PSDB; AAT38466.
XX Ancylostoma caninum secreted protein - useful as antigen for
PT hookworm vaccine prodn.
XX
XX Claim 2; Page 42-43; 66pp; English.
XX
XX Ancylostoma secreted protein ASP-1 is secreted by canine hookworm
CC larvae as they change from the free-living stage to the parasitic
CC stage. The amino acid sequence of the ASP-1 pro-form (AAW04321) was
CC ded. from a cDNA clone (AAT38466) obtd. from an Ancylostoma caninum
CC L3 larvae cDNA library. ASP-1 represents a family of proteins (see
CC also AAW04322-23) that are highly immunogenic in experimental
CC animals. Recombinant ASP proteins can be produced in a variety of
CC hosts. They can be used in vaccines for hookworm, in the diagnosis
XX of hookworm infection, or to raise antibodies.
XX
SQ Sequence 424 AA;
Query Match 36.6%; Score 265.5; DB 17; Length 424;
Best Local Similarity 32.5%; Pred. No. 7,4e-19;
Matches 62; Conservative 27; Mismatches 71; Indels 31; Gaps 6;
OY 7 CQQRKLDMMREMTLHNGYRAAFARNY-----KTSKRTVYDCTLEEKAYK 56
DB 227 CPSNTGMDSVRDFTLSVHNEFRSSVARGLEPDALGNAKRAKMLKMYDDEVASAIR 286
OY 57 SAKESESESESESE---NDVFSATLTNI-----PLEAGNSWMSRIF-----LRG 99
DB 287 HGKTCYQHSNGEDRPGDGENITKTSVLFKDKNAKAQASGLMNNELKEFGVPSNVLT 346
OY 100 KYVNNKNG-KTGINAMVWDSDHKLGAAYVDCSGKTHVVCQYPEAKGDDKTIYEGAPCS 158
DB 347 ALMNRGQMGIGHYTGQAMMDTITKLGCAVYFCNDFFVGCYQPGQNMGMHYITMGQCS 406
OY 159 RGSDDGAGATC 169
DB 407 QCS---PGATC 414
RESULT 28
AAW04322 standard; Protein; 218 AA.
XX
XX AAW04323;
XX
XX 17-JAN-1997 (first entry)
XX
XX Ancylostoma secreted protein ASP-2 type I.
XX
XX Ancylostoma secreted protein; ASP-2; hookworm; vaccine.
XX
XX Ancylostoma caninum.
XX
XX WO9632479-A1.
XX
XX 17-OCT-1996.
XX
XX 10-APR-1996; 96WO-US04821.
XX
XX 10-APR-1995; 95US-0419414.
XX
XX (UYVA) UNIV YALE.
XX
XX Hawdon JM, Hotez PJ, Jones BF;
XX
XX WPI; 1996-477130/47.
XX
XX N-PSDB; AAT38467.
XX
XX Ancylostoma caninum secreted protein - useful as antigen for
PT hookworm vaccine prodn.

XX Claim 2; Page 49-50; 66pp; English.
PS
XX
XX Ancylostoma secreted protein ASP-2 type I (AAW04322) is secreted by
CC canine hookworm larvae as they begin feeding. Its amino acid
CC sequence was deduced from a cDNA clone (AAT38467) isolated from an
CC Ancylostoma caninum L3 larvae cDNA library. Type I ASP-2 differs
CC from type II ASP-2 (AAW04323) only at amino acid positions 92 and 95.
CC The proteins are members of a family of proteins (see also AAW04321)
CC that are highly immunogenic in experimental animals. Recombinant
CC ASP proteins can be produced in a variety of hosts. They can be
CC used in vaccines for hookworm in the diagnosis of hookworm
XX infection, or to raise antibodies.
XX
SQ Sequence 218 AA;
Query Match 26.3%; Score 262; DB 17; Length 218;
Best Local Similarity 30.4%; Pred. No. 6,7e-19;
Matches 58; Conservative 38; Mismatches 69; Indels 26; Gaps 5;
OY 13 LDDDMREMTLHNGYRAAFARNY-----KTSKRTVYDCTLEEKAYSAKCS 62
DB 27 WDEARQKFLDVHNSRSMVAKQAQKDAISGNAPKAKKKKMYDCNVESTAQMNARKCV 86
OY 63 EEPSESE---ENDVFSATLTNI-----PLEAGNSWMSRIF-----ELRGKYNNKNGKT 108
DB 87 FAHSRKGQVGENIMWSTARQMDKAQAQASDGFSELAHYGVGOENLITQLNRCVMT 146
OY 109 SNIAMVWDSDHKLGAAYVDCSGKTHVVCQYPEAKGDDKTIYEGAPCSRDYAGATV 168
DB 147 GHYTMWQESYKLGCVEMCSTMVYGVCYSPQGNMMSLIYERGNPCTKSDSCSNAS 206
OY 169 CDDDMQNLICI 179
DB 207 CSAG--EALCY 215
RESULT 29
AAW04323 standard; Protein; 218 AA.
XX
XX AAW04323;
XX
XX 17-JAN-1997 (first entry)
XX
XX Ancylostoma secreted protein ASP-2 type II.
XX
XX Ancylostoma secreted protein; ASP-2; hookworm; vaccine.
XX
XX Ancylostoma caninum.
XX
XX WO9632479-A1.
XX
XX 17-OCT-1996.
XX
XX 10-APR-1996; 96WO-US04821.
XX
XX 10-APR-1995; 95US-0419414.
XX
XX (UYVA) UNIV YALE.
XX
XX Hawdon JM, Hotez PJ, Jones BF;
XX
XX WPI; 1996-477130/47.
XX
XX N-PSDB; AAT38468.
XX
XX Ancylostoma caninum secreted protein - useful as antigen for
PT hookworm vaccine prodn.
XX
XX Claim 2; Page 51; 66pp; English.
XX
XX Ancylostoma secreted protein ASP-2 type II (AAW04323) is secreted by
CC canine hookworm larvae as they begin feeding. Its amino acid

PA (UYUT-) RIKKSUNITV UTRCHT.
 XX
 PI Cornelissen AMCA, Schallig HDEH;
 XX
 DR WPI: 1998-101048/09.
 DR N-PSDB; AAV03016.
 XX
 XX Polynucleotide encoding excretory secretory trichostrongylid
 PT proteins - ES15 or ES24 of Haemonchus contortus or ES14.0 or ES14.2
 PT of Cooperia oncophora, useful for vaccines against gastro-intestinal
 PT nematodes
 XX
 PS Claim 5; Page 26; 42pp; English.
 XX
 CC This polypeptide comprises the excretory secretory (ES)
 CC trichostrongylid protein ES24 of the gastro-intestinal nematode
 CC Haemonchus contortus. Its amino acid sequence was deduced from a
 CC cDNA clone (see AAV03016) isolated from an L3 larval cDNA library.
 CC Also claimed is a recombinant ES24 polynucleotide comprised in
 CC a vector, and a vaccine for combatting H. contortus infections in
 CC sheep or goats that comprises the recombinant polynucleotide or the
 CC ES24 protein. Vaccines are also provided that contain or express
 CC the ES15 protein (see AAV37165) of H. contortus or the ES14.0 (see
 CC AAV37167) or ES14.2 (see AAV37168) antigen in ruminant production.
 CC Trichostrongylids are a major constraint in ruminant production
 CC world-wide, e.g. producing diarrhoea or anaemia leading to reduced
 CC milk, meat and wool production. To enhance immunogenicity, the ES
 CC polypeptides can be used as homopolymers, hetero-polymers, or
 CC coupled with other compounds, e.g. adjuvants.
 XX
 SO Sequence 222 AA;
 Query Match 21.5%; Score 214; DB 19; Length 222;
 Best Local Similarity 28.0%; Pred. No. 6.6e-14;
 Matches 58; Conservative 28; Mismatches 89; Indels 32; Gaps 8;
 QY 2 GDYSICQOREKLDNREKFTELHNGYRAAFARY-----KTSKRTMYDCT 49
 DB 17 GHAASCPTDGMDEVRQTFVKNHAYRTLVAKGEKNAKEIGYAPPAAMLYVDDA 76
 QY 50 LEKRAYSAKRC--SEEPSSEEN--VDVESAATLN-----IPLDAGNSWSEIFELRCK 100
 DB 77 IEEENTMFARKCYFAHNSYSESNMGNOLYWTSTILNONTVAALAESVDLMFDEL-QONGCV 135
 QY 101 VYNK-----NGKTSINIANMYWDSHDKGCAVVDSCGKTHVVCYGEPEAKGDKTYEE 153
 DB 136 PTDNYMTMAVFNRGVGHYQYVWQMSNKGCAVEMCSDMTFVACPEYDSAGYMGMPTEY 195
 QY 154 GAPCRCSGYG-AGVYCDDDMONLICI 179
 DB 196 GNPCTNNEDCKCTNCVCSRD--EALCI 220
 RESULT 34
 ID AAR26785 standard; Protein; 454 AA.
 AC AAR26785;
 XX
 DT 26-JAN-1993 (first entry)
 DE Sequence of a homologue of the 45 kd antigen encoded by
 DE pBTA879.
 XX
 KM Antigen; vaccine; parasitic nematode; immunogen.
 XX
 OS Haemonchus contortus.
 XX
 FH Key Location/Qualifiers
 FT 22..42
 FT Region /note- "homologous to 45 kd protein"
 FT 253..273
 FT /note- "see above"

FT Region 274..287
 FT /note- "homologous with Endoproteinase Lys-C
 FT peptide"
 FT 302..0
 FT Region /note- "as above"
 XX
 PN M09213889-A.
 XX
 PD 20-AUG-1992.
 XX
 PE 06-FEB-1992; 92MO-AU000040.
 XX
 PK 06-FEB-1991; 91AU-0004486.
 XX
 PA (BIOT-) BIOTEC AUSTRALIA PTY LTD.
 XX
 PI Cobon GS, Sharp PJ, Wagland BM;
 XX
 DR WPI: 1992-289990/36.
 DR N-PSDB; AAQ28093.
 XX
 PT Vaccines comprise antigens derived from parasitic nematodes -
 PT useful for passive immunisation against round, whip, filariasis,
 PT thread and hookworms on host
 XX
 PS Claim 15; Fig 7; 86pp; English.
 XX
 CC PCR primers A112/301 and A112/302 were designed to be used to
 CC amplify the DNA encoding the 45 kd protein. In the reaction
 CC containing primer A112/301 a unique band of approximately 650 bp was
 CC observed. The approximately 650 bp band was not seen when primer
 CC A112/302 was used. The PCR cloned was grown and purified for use as
 CC a hybridisation probe to screen the pBTA879 cDNA library. pBTA879
 CC is the sequence of one of these clones. There is no methionine
 CC initiation codon present in this region of the sequence so this clone
 CC probably does not represent the complete coding region. pBTA879
 CC identical to, the native glycoprotein which is related to, but not
 CC identical to, the native glycoprotein isolated from H. contortus.
 CC 45 kd antigen, cDNA libraries were screened with the fragment
 CC isolated from pBTA879. AAQ28094 is the sequence of one of these
 CC clones, pBTA 963. Once again, this clone does not contain an
 CC initiation methionine.
 XX
 SO Sequence 454 AA;
 Query Match 20.6%; Score 205; DB 13; Length 454;
 Best Local Similarity 28.5%; Pred. No. 1.6e-12;
 Matches 55; Conservative 36; Mismatches 74; Indels 28; Gaps 8;
 QY 13 LDDNREKFTELHNGYRAAFARY-----KTSKRTMYDCTLEKRAYSAKCS 62
 DB 262 MTDKARKHFDVKNHEYSILAKQAKRPGQAPKAAHAKAYVDCDDEANMEKSTCT 321
 QY 63 EEPSSSE-----ENVVESAATLN-----IPLDAGNSWSEIFEL--RKYNNKGT-- 108
 DB 322 FGLNTAMAKTKRGNMNMSSKANNTETAALAEAVAAWFGDLQRYGVPENNVFTMNVTTL 381
 QY 109 SNTANKVWDSHDKGCAVYDC-SGKTHVVCYGEPEAKGDKTYEGAPCRCSGYGA-G 166
 DB 382 SKYSQLANQSSDRIGCVVPCWMSMTVYVCEYNGDLPALAYDVGDCYKADCCPG 441
 QY 167 VTCDDMONLICI 179
 DB 442 CTCRSR--EGLCV 452
 RESULT 35
 ID AAR26786 standard; Protein; 440 AA.
 AC AAR26786;
 XX
 AC AAR26786;

[illegible]

. 185 DIGDPG-----TTDEMQ--CTG 200

RESULT 36
AAK52990
AAK52990 standard; Protein; 189 AA.

XX AAK52990;
XX 0Z-JUN-1994 (first entry)
XX Canine hookworm Neutrophil Inhibitory Factor isoform 6FL.
XX DE neutrophil inhibitory factor; NIF; glycoprotein; endoparasite;
XX KW nematode; parasitic worm; canine hookworm; peritoneal inflammation.
XX OS Ancylostoma caninum.
XX MO9323063-A.
XX PN 25-NOV-1993.
XX PD 11-MAY-1993; 93MO-0504502.
XX PF 11-MAY-1992; 92US-0881721.
XX PR 24-DEC-1992; 92US-0996972.
XX PA (CORV-) CORVAS INT INC.
XX PI Foster DL, Moyle M, Vlasak GP;
XX DR WPI; 1993-386208/48.
XX PT New neutrophil inhibitory factor from parasitic worms - for
XX preventing and treating inflammation, also derived nucleic acid,
XX vectors, transformed hosts and antibodies
XX Example 10; Fig 9; 114pp; English.
XX PS

A canine hookworm cDNA library was screened with a probe amplified
using primers 30.2 and 43.3.RC(AA052476 and AA052477, respectively)
which were based on sequences of isolated NIF peptide fragments. Seven
of the 120 positive clones were isolated for sequence analysis. One
clone, designated clone 1FL, encoded an 825 nucleotide open reading
frame (AA052475). The other clones contained partial ORFs and coded
partial NIF polypeptides (see AAK52985-52990) which are thought to
represent six NIF isoforms that are significantly similar but
not identical to, the prototypical NIF-1FL polypeptide (AAK42488).

Sequence 189 AA;

DB 20.1%; Score 200; DB 14; Length 189;
Query Match 32.9%; Pred. No. 1,5e-12;
Best Local Similarity 16; Mismatches 46; Indels 40; Gaps 6;
Matches 50; Conservative 16; Mismatches 46; Indels 40; Gaps 6;

15 DDMRMFTELHNGCYRAAFARNY-----KTSKNRPMYYDCT 49
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
40 DSIRLQGLFAHNHGNYRNALGHIGISKEIDGDYDDYYFYFSAPAMASRYLEKDCD 99
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
50 LEEKAYSARKCEE---PSEERNDVF-SAAATNITPLEAGN---SWMSRIPEL---- 97
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
100 SRSASYMSASKCDSSSPFGIDENKYILSENSIN---EARRLATISSGKEAFNLNETG 156
98 RGRVYNKNGKTSNIAMMYGDSHDICGAVYDC 129
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
157 EGVLYRSLTILSNPNAMDIREKFGCAVVKC 188

RESULT 37
AAI23598
AAI23598 standard; Protein; 189 AA.

XX AAI23598;
XX

XX Lustigman S, Peatman E, Unnisch TR;
 XX WPI: 2001-662950/76.
 XX
 PT Inducing angiogenesis in a tissue using the Ov-ASP protein isolated
 PT from the nematode *Onchocerca volvulus* is useful to treat circulatory or
 PT vascular disease such as ischemia
 XX
 PS Claim 1: Fig 1: 37pp: English.
 XX
 CC The present invention relates to a method for inducing angiogenesis in a
 CC tissue. The method comprising contacting the tissue with Ov-ASP. The Ov-
 CC ASP molecules are used to treat circulatory or vascular disorders,
 CC particularly ischemia, congenital heart disease, myocardial disease or
 CC peripheral disease, more particularly cerebrovascular ischemia, veno-
 CC occlusive disease or myocardial ischemia, especially coronary artery
 CC disease. The invention is also used to treat cancer, diabetic
 CC retinopathy and inflammatory disease. Angiogenesis is also central to a
 CC number of pathological processes, including abnormalities of wound
 CC healing in diseases such as diabetes and duodenal ulceration; chronic
 CC inflammatory disorders such as rheumatoid arthritis, psoriasis and
 CC periodontitis; dermatological conditions such as cutaneous malignancy,
 CC Kaposi's sarcoma, pyogenic granulomas and warts. Anti-Ov-ASP factors are
 CC useful to treat onchocerciasis (River Blindness) or benign or malignant
 CC neoplasia. The present sequence is *Onchocerca volvulus* (Ov)-ASP-1
 CC protein.
 XX
 SQ Sequence 223 AA:
 XX
 Query Match 16.2%; Score 161.5; DB 22; Length 223;
 Best Local Similarity 25.9%; Pred. No. 1.9e-08;
 Matches 53; Conservative 28; Mismatches 73; Indels 51; Gaps 11;
 XX
 QY 9 QREKLDDEKREFTLHNGYRAAFARNY--KTSKRTWVYDCTEEAYKSK-SEE 64
 DB 28 ERKKIVGQNNKRRSLINGKLKNGYPRKNNLELRMKCLESSAQKMANOCIFGHS 87
 QY 65 PSSEENV--DYF-----SAATLPIPEAENSWSEIFELGKYNNNGTS 109
 DB 88 PROGRGVEENVYAVWSVSVEGLKTAGT-----DAGKSWMSL-----PKLY-ENNSN 137
 QY 110 NI-----ANWYDSHKLICAY-VVCSG--KTHVYCYGPEAKGSKGTYEES 154
 DB 138 NMTKVAAGGVLAHRTQAMMGKTYKIGGVAATCGDGRLLVICHYSPGSMGVEITYRG 197
 QY 155 APCRSQSDGAGVTCDDDMNLICI 179
 DB 198 NPCNPK-----VDKCYTKKCL 215
 XX
 RESULT 41
 AA008687
 ID AA008687 standard; Protein: 300 AA.
 XX
 AC AA008687;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human FCRT7 polypeptide sequence.
 XX
 KW Human: FCRTX; myelogenous leukaemia; carcinoma; melanoma; glioma;
 KW astrocytoma; congenital neonatal alloimmune thrombocytopenia; infection;
 KW neurological disorders; neurodegenerative disorders; nerve trauma;
 KW familial myelodysplastic syndrome; Charcot-Marie-Tooth neuropathy;
 KW demyelinating Gardner syndrome; familial myelodysplastic syndrome;
 KW mental health condition; immunological disorder; allergy; infertility;
 KW bronchial asthma; Avelino type eosinophilia; lung disease; deafness;
 KW reproductive disorder; reproductive disorder; glycoprotein Ia deficiency;
 KW desmoid disease; turcot syndrome; liver cirrhosis; hepatitis C; vituicide;
 KW gastritis; pancreatic disease; Schistosoma mansoni infection;
 KW spinocerebellar ataxia; Plasmodium falciparum parasitaemia; diabetes;
 KW Corneal dystrophy; Greenow type I; Corneal dystrophy-lattice type I;

KW Reis-Bucklers corneal dystrophy; cytostatic; immunosuppressive;
 KW antidiabetic; antistimulant; antileptin; antileptin; antileptin;
 KW antidiabetic; protoscoler; hepatotropic; vituicide; ophthalmological;
 KW gynaecological; antifertility; immunostimulant; auditory; haemostatic;
 KW gene therapy; FCRT7; trypsin inhibitor-like protein.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT MISC-difference 102
 FT /note- "Encoded by AT"
 XX
 XX MO20016747-A2.
 XX
 XX 13-SEP-2001.
 XX
 XX 05-MAR-2001; 2001MO-US07160.
 XX
 XX 03-MAR-2000; 2000US-186592P.
 XX 03-MAR-2000; 2000US-186718P.
 XX 06-MAR-2000; 2000US-187293P.
 XX 06-MAR-2000; 2000US-187294P.
 XX 17-MAR-2000; 2000US-190400P.
 XX 07-APR-2000; 2000US-196018P.
 XX 03-JAN-2001; 2001US-259548P.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 XX Vernet CAM, Fernandes E, Shimkets RA, Herrmann JL, Majumder K;
 XX Macdougall J, Mishra V, Mezes PS, Rastelli L,
 XX WPI: 2001-596837/67.
 XX N-PSDB: AMS14095.
 XX
 XX Novel polypeptides designated as FCRTX polypeptides, useful in
 XX detection, prevention and treatment of a broad range of pathological
 XX states
 XX
 PS Claim 1: Page 111; 215pp: English.
 XX
 CC The invention relates to human FCRTX polypeptides, FCRT1-FCRT7, and the
 CC nucleic acids encoding them. These sequences are useful for the treatment
 CC or prevention of numerous disorders including myelogenous leukaemia,
 CC carcinoma, melanoma, glioma, astrocytoma, congenital neonatal
 CC alloimmune thrombocytopenia, neurological disorders, neurodegenerative
 CC disorders, nerve trauma, familial myelodysplastic syndrome,
 CC Charcot-Marie-Tooth neuropathy, demyelinating Gardner syndrome, familial
 CC myelodysplastic syndrome, mental health conditions, immunological
 CC disorders, allergy and infection, bronchial asthma, Avelino type
 CC eosinophilia, lung diseases, reproductive disorders, infertility, male
 CC and female reproductive disorders, deafness, glycoprotein Ia deficiency,
 CC desmoid disease, turcot syndrome, liver cirrhosis, hepatitis C, gastric
 CC disorders, pancreatic diseases such as diabetes, Schistosoma mansoni
 CC infection, spinocerebellar ataxia, Plasmodium falciparum parasitaemia,
 CC Corneal dystrophy Greenow type I, Corneal dystrophy-lattice type I and
 CC Reis-Bucklers corneal dystrophy. This sequence represents FCRT7, a
 CC trypsin inhibitor-like protein.
 CC
 XX
 SQ Sequence 300 AA:
 XX
 Query Match 16.0%; Score 160; DB 22; Length 300;
 Best Local Similarity 25.5%; Pred. No. 4.2e-08;
 Matches 53; Conservative 31; Mismatches 66; Indels 58; Gaps 11;
 XX
 QY 1 EGDYSIQQREK---LDDMKREMTLHNGYRAAFARNKT-SKRTWVYDCTLEAKYK 56
 DB 43 DGEWIMKQKGRKATTDNDOSIL-DLHNLIR---SOYFPAASNNKEMTVDLELSAES 98
 QY 57 SAECSE--PSSEENVYVSATLTIPLAG-----NSMASEI----- 94
 DB 99 RAESCIMHEHPAS-----LLPSTGOMLGAMGRYRPPFTFVQSMYDEVDSYPYHEHC 152
 QY 95 -----FELNKKYNNKNGTSNIAMWDSHDKLGCAVYDSCG-----KTHVCOY 139

```

DB 153 NPYPCFPCSGPY-----CTHTQVWATSNKRGALNLCNNMIMQIIPKAVLYLCWY 206
OY 140 GPEAKGDGKTYEBGAPCSRC-SDYGAG 166
DB 207 SPKGNMNGHAPYKHGCPSCAPSPFGGG 234

RESULT 42
AAM39716
ID AAM39716 standard; Protein; 266 AA.
AC AAM39716;
XX 22-OCT-2001 (first entry)
DE Human polypeptide SEQ ID NO 2861.
XX
XX Human; nocitropic; immunosuppressant; cytosstatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokine; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.
XX
XX Homo sapiens.
XX
XX MO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000OW-0534263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX Zhao OA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
XX N-PSDB: AAI58872.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries -
XX
XX Example 4; SEQ ID NO 2861; 10078bp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and
XX the encoded polypeptides (AAM38642-AAM42213) with nocitropic,
XX immunosuppressant and cytosstatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening
XX assays for receptor activity, arthritis and inflammation, leukaemia and
XX C.N.S disorders.
XX
XX Note: The sequence data for this patent did not form part of the printed
XX specification.

```

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SQ Sequence 266 AA:
Query Match 15.9%; Score 159; DB 22; Length 266;
Best Local Similarity 28.6%; Pred. 4.5e-08;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

OY 13 LDDREMEFTELHNGRAAFARNYKTSKRTMYDCTLEBKAYSAERC-----SEPPSS 68
DB 28 LIDEERKRLMVELHNLVRAQVSP--ASDMLHMRWDELAFAKAYAROCVGNHKKRGR 85
OY 69 EENVDFESAATLNIPLDAGNSWMSSEIFELNGKYVNNKGTSTNIANN-----VMDSHDK 121
DB 86 GENLFAITDEGMDVPL-AMEEWHNE-----REHYNLSAATCSPGCMCGHYQVWAKTER 139
OY 122 LGCAYVDCS-----GKTHV---VCOYGEPAKGDGKTYEBGAPCSRCSDYGAGVTCDDW 173
DB 140 ICGSHFCEKIQGEVEETNIELVNCYEPGKVRKRPYQEGTSCSCP---SGYHC---- 192
OY 174 ONILC 178
DB 193 KNSLC 197

RESULT 43
AAM41502
ID AAM41502 standard; Protein; 347 AA.
AC AAM41502;
XX
XX 22-OCT-2001 (first entry)
DE Human polypeptide SEQ ID NO 6433.
XX
XX Human; nocitropic; immunosuppressant; cytosstatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokine; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.
XX
XX Homo sapiens.
XX
XX MO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000OW-0534263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX Zhao OA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
XX N-PSDB: AAI60658.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries -
XX
XX Example 2; SEQ ID NO 6433; 10078bp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and
XX the encoded polypeptides (AAM38642-AAM42213) with nocitropic.

```

CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilization of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

CC Sequence 347 AA:

Query Match 15.98; Score 159; DB 22; Length 347;
 Best Local Similarity 28.68; Pred. No. 6.5e-08;
 Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

OY 13 LDDDMEMETLHNGCYAPAFARVYKSKRMVYDCLEKAKSKERC---SEPSSE 68
 DB 105 LTDEERKLVNLTNLYRQVSP--ASDMLHMDDELAFAYARQVWGHNRKGR 162
 OY 69 EENVDFSAATNPIELRGSWSEFELRGVYKNGKTSNIAH-----VWDSHK 121
 DB 163 GEMFATIDEGMDVPLAMEEMHE-----KEHILSAICSFGOCGHITVWAKTER 216
 OY 122 LCAVAVDCS-----GKTHV---VCOYGPAAKDGKTIYEGARCSGYGAVTCDDW 173
 DB 217 IGGGSHFCKLQGVETRIELVCEHPEGNVKGRRPDEKPCSCP---SGHIC--- 269
 OY 174 QNLIC 178
 DB 270 KNSLC 274

RESUME 44

AA113392
 ID AA113392, standard; Protein: 463 AA.

AC AA113392;

DT 25-JUN-1999 (first entry)

XX Amino acid sequence of protein PRO328.

XX Secreted protein; transmembrane protein; human; enterocolitis;
 KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
 KW congenital microvillus atrophy; skin disease; cell growth;
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
 KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
 KW fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
 KW anti-thrombotic; wound healing; tissue repair.

OS Homo sapiens.

XX WO9914328-A2.

PN 25-MAR-1999.

PD 16-SEP-1998; 98WO-0519330.

XX 25-NOV-1997; 97US-0066840.

PR 17-SEP-1997; 97US-0059113.

PR 17-SEP-1997; 97US-0059115.

PR 17-SEP-1997; 97US-0059117.

PR 17-SEP-1997; 97US-0059121.

PR 17-SEP-1997; 97US-0059122.

PR 17-SEP-1997; 97US-0059184.

PR 18-SEP-1997; 97US-0059263.

PR 18-SEP-1997; 97US-0059266.
 PR 15-OCT-1997; 97US-0062125.
 PR 17-OCT-1997; 97US-0062285.
 PR 17-OCT-1997; 97US-0062287.
 PR 21-OCT-1997; 97US-0063486.
 PR 24-OCT-1997; 97US-0062814.
 PR 24-OCT-1997; 97US-0062816.
 PR 24-OCT-1997; 97US-0063045.
 PR 24-OCT-1997; 97US-0063120.
 PR 24-OCT-1997; 97US-0063121.
 PR 24-OCT-1997; 97US-0063127.
 PR 24-OCT-1997; 97US-0063128.
 PR 27-OCT-1997; 97US-0063329.
 PR 27-OCT-1997; 97US-0063327.
 PR 28-OCT-1997; 97US-0063541.
 PR 28-OCT-1997; 97US-0063544.
 PR 28-OCT-1997; 97US-0063549.
 PR 28-OCT-1997; 97US-0063550.
 PR 28-OCT-1997; 97US-0063564.
 PR 29-OCT-1997; 97US-0063435.
 PR 29-OCT-1997; 97US-0063704.
 PR 29-OCT-1997; 97US-0063732.
 PR 29-OCT-1997; 97US-0063738.
 PR 29-OCT-1997; 97US-0063739.
 PR 29-OCT-1997; 97US-0063735.
 PR 31-OCT-1997; 97US-0063730.
 PR 31-OCT-1997; 97US-0064102.
 PR 03-NOV-1997; 97US-0064248.
 PR 07-NOV-1997; 97US-0064809.
 PR 12-NOV-1997; 97US-0065186.
 PR 17-NOV-1997; 97US-0065846.
 PR 18-NOV-1997; 97US-0065932.
 PR 21-NOV-1997; 97US-0066120.
 PR 21-NOV-1997; 97US-0066364.
 PR 24-NOV-1997; 97US-0066772.
 PR 24-NOV-1997; 97US-0066466.
 PR 24-NOV-1997; 97US-0066770.
 PR 24-NOV-1997; 97US-0066511.
 PR 24-NOV-1997; 97US-0066453.

(GENTH) GENENTECH INC.

XX Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;

XX WPI; 1999-229533/19.

XX N-PSDB; AAX52263.

XX New isolated human genes and polypeptides used in, e.g. treatment of
 gastrointestinal ulceration

XX Claim 12; Fig 100; 320pp; English.

XX AA113344-403 represent secreted and transmembrane human proteins.
 CC The cDNA sequences are obtained from cDNA libraries, prepared from
 CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.
 CC The encoded polypeptides have specific uses based on their homology to
 CC known polypeptides, e.g. PRO211 and PRO217 can be used for disorders
 CC associated with the preservation and maintenance of gastrointestinal
 CC mucosa and the repair of acute and chronic mucosal lesions
 CC (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal
 CC ulceration and congenital microvillus atrophy), skin diseases associated
 CC with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial
 CC cancers such as lung squamous cell carcinoma of the vulva and gliomas),
 CC potent effects on cell growth and development, diseases related to
 CC growth or survival of nerve cells including Parkinson's disease,
 CC Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as
 CC for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used
 CC of Usher Syndrome or Atrophia areata. PRO263 may be used in the treatment
 CC anti-thrombotic agent. PRO287 polypeptides and portions may have
 CC therapeutic applications in wound healing and tissue repair; PRO317 can

CC be used for treating problems of the kidney, uterus, endometrium, blood
 CC vessels, or related tissue, e.g. in the heart of genital tract.

XX Sequence 463 AA;

Query Match 15.9%; Score 159; DB 20; Length 463;

Best Local Similarity 28.6%; Pred. No. 9,8e-08;

Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

```

OY 13 LDDMRMFTELHNGYRAFAFANKYTKMRTYDCTLEKAYKSARK-----SEEPSE 68
DB 28 LTDEKRLAYELHNLVRAQVPT--ASDMLHMDSELAAPAKAYACVWGHNKRGRR 85
OY 69 EBNVDSATLNTPIPEAGNSWSEIFELGRKYNNNGKSTIANM-----YVDSHDK 121
DB 86 GENFATIDGMDVPL-AMEWHNE-----REHYNLSATCSPOKCGHTQYVAKTER 139
OY 122 LGCANVDCS-----GKTHV---VCGYPEAKGKGGKTYPEAGPSRCSDDGAGTCDDDW 173
DB 140 IGGSHFCERKLGVEETNELVNCNPERPGNVKGRPRYEGSPGCP---SGYHC---- 192
OY 174 ONLTC 178
DB 193 KNSIC 197

```

RESULT 45

AA01373 standard; Protein; 463 AA.

AA01373;

20-OCT-2000 (first entry)

Neuron-associated protein.

Neuron associated protein; NEUAP; neurological disorder; epilepsy;
 Ischemic cerebrovascular disease; stroke; cerebral neoplasm;
 Alzheimer's disease; Pick's disease; Huntington's disease;
 dementia; Parkinson's disease; demyelinating disease; meningitis;
 Prion disease; Kuru; Creutzfeldt-Jakob disease; neurofibromatosis;
 cerebral palsy; muscular dystrophy; central nervous system; CNS;
 peripheral nervous system; PNS; myopathy; schizophrania;
 actinic keratosis; arteriosclerosis; atherosclerosis; burralls;
 Kuru; Kuru; paroxysmal nocturnal haemoglobinuria; cancer;
 autoimmune disease; inflammation; acquired immunodeficiency syndrome;
 AIDS; Addison's disease; adult respiratory distress syndrome;
 allergy; ankylosing spondylitis; amyloidosis; anaemia; asthma;
 Werner syndrome; trauma; human.

Homo sapiens.

Location/Qualifiers

1..27 /label= Signal peptide

Disulfide-bond 5 /note= "Potential disulfide bond forming residue"

Modified-site 29 /note= "Potential phosphorylation site"

Modified-site 50 /note= "Potential phosphorylation site"

Disulfide-bond 74 /note= "Potential phosphorylation site"

Modified-site 114 /note= "Potential disulfide bond forming residue"

Disulfide-bond 120 /note= "Potential glycosylation site"

Disulfide-bond 126 /note= "Potential disulfide bond forming residue"

Modified-site 137 /note= "Potential disulfide bond forming residue"

Disulfide-bond 142 /note= "Potential phosphorylation site"

FT Disulfide-bond 147 /note= "Potential disulfide bond forming residue"

FT Modified-site 156 /note= "Potential disulfide bond forming residue"

FT Disulfide-bond 163 /note= "Potential phosphorylation site"

FT Disulfide-bond 186 /note= "Potential disulfide bond forming residue"

FT Disulfide-bond 192 /note= "Potential disulfide bond forming residue"

FT Disulfide-bond 195 /note= "Potential disulfide bond forming residue"

FT Disulfide-bond 197 /note= "Potential phosphorylation site"

FT Disulfide-bond 202 /note= "Potential disulfide bond forming residue"

FT Modified-site 218 /note= "Potential phosphorylation site"

FT Modified-site 227 /note= "Potential phosphorylation site"

FT Modified-site 283 /note= "Potential phosphorylation site"

FT Disulfide-bond 283 /note= "Potential disulfide bond forming residue"

FT Modified-site 299 /note= "Potential phosphorylation site"

FT Modified-site 323 /note= "Potential phosphorylation site"

FT Modified-site 394 /note= "Potential phosphorylation site"

FT Modified-site 403 /note= "Potential phosphorylation site"

FT Modified-site 409 /note= "Potential glycosylation site"

FT Modified-site 409 /note= "Potential glycosylation site"

PN W0200034477-A2.

XX 15-JUN-2000.

XX 10-DEC-1999; 99W0-US30408.

XX 11-DEC-1998; 98US-0210083.

XX 11-DEC-1998; 98US-9123456.

PR 09-FEB-1999; 99US-0119365.

PR 16-MAR-1999; 99US-0124687.

XX (INCY-) INCYTE PHARM INC.

XX Tang YT, Yue H, Baughn MR, Hillman JL, Lal P, Au-young J, Yang J;

PI Lu DM, Azimzal Y;

XX WPI; 2000-423423/36.

XX N-PSDB; AAA47414.

DR New human neuron-associated proteins and polynucleotides encoding them,

XX useful for diagnosis, treatment and prevention of cell proliferative

XX disorders including cancer, neuronal and neurological disorders

PS Claim 1; Page 94-95; 145pp; English.

XX Human neuron-associated proteins (NEUAP) can be used for

CC treating or preventing a disorder associated with decreased

CC expression or activity of NEUAP. Antagonists of NEUAP are useful for

CC treating or preventing disorder associated with increased expression

CC or activity of NEUAP. NEUAP or their fragments or derivatives are

CC useful for treating neurological disorder such as epilepsy, ischemic

CC cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's

CC disease, Pick's disease, Huntington's disease, dementia and

CC Parkinson's disease. NEUAPs are also useful for treating other

CC demyelinating diseases, bacterial and viral meningitis, prion

CC diseases including kuru, Creutzfeldt-Jakob disease, nutritional and

CC metabolic diseases of the nervous system, neurofibromatosis, other

CC developmental disorders of the central nervous system, cerebral

CC palsy, neuroskeletal disorders, autonomic nervous system disorders,

CC cranial nerve disorders, spinal cord diseases, muscular dystrophy and
CC other neuromuscular disorders, peripheral nervous system disorders,
CC inherited, metabolic, endocrine and toxic myopathias, mental
CC disorders including mood, anxiety and schizotypic disorders, a cell
CC proliferative disorder such as actinic keratosis, arteriosclerosis,
CC thierosclerosis, buritis, cirrhosis, hepatitis, mixed connective
CC tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal
CC haemoglobinuria, cancers of the adrenal gland, bladder, bone,
CC bone marrow, brain, breast, cervix, and an autoimmune/inflammatory
CC disorder such as acquired immunodeficiency syndrome (AIDS), Addison's
CC disease, adult respiratory distress syndrome, allergies, ankylosing
CC spondylitis, amyloidosis, anemia, asthma, Werner syndrome,
CC complications of cancer, hemodialysis, and extracorporeal circulation,
CC viral, bacterial, fungal parasitic, protozoal, and helminthic
CC infections, and trauma. This protein was given the Incyte ID no.
CC 2634931CD1.

XX
SQ Sequence 463 AA;

Query Match 15.98; Score 159; DB 21; Length 463;

Best Local Similarity 28.68; Pred. No. 9,8e-08;

Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

OY 13 LDDDMREMTLHNGYNAFAFARNYKTSKMTWYDCTLEKAYKSAEC---SEEPSSE 68
DB 28 LTDEERKLAVELHNLRYAQSPT--ASDMLHMRNDEELAAFAKAYARQCVMGHNREGR 85
OY 69 EENVDFSAATLNIPLDAGNSWSEIFELRGKVYKNGKTSNIANN-----VWDSHDK 121
DB 86 GEMLFALITDEGMDVPL-AMEEWHE-----REHYNLSPAATCSPGOMCGHYTOVWAKTER 139
OY 122 LGCAYVDCS-----GKTHV---VCQYGPFAKGDGKTIYEGAPCSRSDYGAGVTCDDDW 173
DB 140 IGGGSHFEKLGVEETNIELVNCNEPFGNVKGRPRYQEGTFCSCOP---SGYHC----- 192
OY 174 QNLIC 178
DB 193 KNSLIC 197

Search completed: July 15, 2003, 08:36:12
Job time : 73 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 08:32:08 ; Search time 26 Seconds

(without alignments)
204.829 Million cell updates/sec

Title: us-09-937-555a-2

Perfect score: 997
Sequence: 1 EGVSYLCQQRERKIDDDHREK.....DYAGACTCDDDDMONTLCIGH 181

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued Patents, AA.*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/BACKFILES1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	299	30.0	231	1	US-08-173-510B-86 Sequence 86, App1
2	299	30.0	231	1	US-08-458-218-84 Sequence 84, App1
3	299	30.0	231	2	US-08-450-497-86 Sequence 86, App1
4	290.5	29.1	232	1	US-08-173-510B-84 Sequence 84, App1
5	290.5	29.1	232	1	US-08-458-218-82 Sequence 82, App1
6	290.5	29.1	232	2	US-08-450-497-84 Sequence 84, App1
7	290	29.1	274	1	US-08-173-510B-83 Sequence 83, App1
8	290	29.1	274	1	US-08-458-218-81 Sequence 81, App1
9	290	29.1	274	2	US-08-450-497-81 Sequence 83, App1
10	266	26.7	224	1	US-08-173-510B-87 Sequence 87, App1
11	266	26.7	224	1	US-08-458-218-85 Sequence 85, App1
12	266	26.7	224	2	US-08-450-497-85 Sequence 87, App1
13	265.8	25.6	224	1	US-08-419-418-2 Sequence 2, App1
14	265	25.6	208	1	US-08-173-510B-85 Sequence 85, App1
15	265	25.6	208	1	US-08-458-218-83 Sequence 83, App1
16	265	25.6	208	2	US-08-450-497-83 Sequence 85, App1
17	205	20.6	434	1	US-07-930-686-10 Sequence 10, App1
18	205	20.6	434	1	US-08-460-998-10 Sequence 10, App1
19	200	20.1	189	1	US-08-173-510B-89 Sequence 89, App1
20	200	20.1	189	1	US-08-458-218-87 Sequence 87, App1
21	200	20.1	189	2	US-08-450-497-89 Sequence 89, App1
22	197.5	19.8	440	1	US-07-930-686-12 Sequence 12, App1
23	197.5	19.8	440	2	US-08-460-998-12 Sequence 12, App1
24	155	15.5	204	5	PCT-US96-07709-33 Sequence 30, App1
25	155	15.5	220	5	PCT-US96-07709-30 Sequence 25, App1
26	155	15.5	248	5	PCT-US96-07709-25 Sequence 1, App1
27	151	15.1	270	2	US-08-773-368-1 Sequence 1, App1

28	151	15.1	270	3	US-09-199-887-1
29	144	14.4	146	1	US-08-173-510B-88
30	144	14.4	146	1	US-08-458-218-86
31	144	14.4	146	2	US-08-450-497-88
32	141	14.1	205	1	US-08-450-944-5
33	141	14.1	205	5	PCT-US96-07709-5
34	141	14.1	221	1	US-08-450-944-2
35	141	14.1	221	5	PCT-US96-07709-2
36	127	12.7	138	2	US-07-857-224B-112
37	122	12.2	266	2	US-08-773-368-4
38	122	12.2	266	2	US-09-199-887-4
39	121	12.1	219	2	US-08-199-887-3
40	121	12.1	219	3	US-09-199-887-3
41	115	11.5	137	2	US-07-857-224B-111
42	112.5	11.3	204	1	US-08-614-935-5
43	112.5	11.3	204	3	US-09-130-287-5
44	110	11.0	205	1	US-08-614-935-4
45	110	11.0	205	3	US-09-130-287-4

ALIGNMENTS

RESULT 1
US-08-173-510B-86
Sequence 86, Application US/08173510B
Patent No. 5747296
GENERAL INFORMATION:
APPLICANT: MATTHEW NOBLE, ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 104
CORRESPONDING ADDRESS:
ADDRESSER: Lyon 8 Lyon
STREET: 633 West Pflin Street
STREET: Suite 1700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 MB
MEDIUM TYPE: Storage
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,510B
FILING DATE: 23-DEC-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOV-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 205/073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
US-08-173-510B-86

Sequence 1, App1
Sequence 88, App1
Sequence 86, App1
Sequence 88, App1
Sequence 5, App1
Sequence 2, App1
Sequence 112, App
Sequence 4, App1
Sequence 3, App1
Sequence 3, App1
Sequence 111, App
Sequence 5, App1
Sequence 4, App1
Sequence 4, App1
Sequence 4, App1

Query Match 30.0%; Score 299; DB 1; Length 231;
Best Local Similarity 35.2%; Pred. No. 4.2e-25;
Matches 74; Conservative 20; Mismatches 58; Indels 58; Gaps 8;

QY 6 LCOQRK-----LDDHMEFTELHNGYRAAFARNY----- 36
DB 16 ICSQNGTGFPGFNDMSKFLFLEHNGYRSLALGHISITEPEPSYDDDDYGYSEVLXAP 75
QY 37 KTSKRTMYDCTTEERAYSAEKCEPSSSE-----BENDVPSAATLNIPLEA 86
DB 76 SASKRTMYEDCEERKSAKSAKSSCDSSSPGYDENKTYLHNSNISEARLAI----- 131
QY 87 GNSWSEIFEL-----RKYVKNKGTSTIANKAWDSDHKLGCAYVDCSK-----THVY 136
DB 132 -LSMAEAFDLNKTGEGVLYRSLTISFNAILAMDTRKFGCAVACPLKDTSATTHVY 190
QY 137 CQYGPBANG--DGKTYEGAPCSRCSYD 163
DB 191 CHY-PRIEGEEREGKQIYKVGTPCGDCSEY 219

RESULT 2
US-08-458-218-84
; Sequence 84, Application US/08458218
; Patent No. 5789178
; GENERAL INFORMATION:
; APPLICANT: MATTHEW MOYLE ET AL.
; TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,218
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/151,064
; FILING DATE: 10-NOVEMBER-1993
; APPLICATION NUMBER: 08/060,433
; FILING DATE: 11-MAY-1993
; APPLICATION NUMBER: 07/881,721
; FILING DATE: 11-MAY-1992
; APPLICATION NUMBER: 07/996,972
; FILING DATE: 24-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 203/226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
US-08-458-218-84

Query Match 30.0%; Score 299; DB 1; Length 231;

Best Local Similarity 35.2%; Pred. No. 4.2e-25;
Matches 74; Conservative 20; Mismatches 58; Indels 58; Gaps 8;

QY 6 LCOQRK-----LDDHMEFTELHNGYRAAFARNY----- 36
DB 16 ICSQNGTGFPGFNDMSKFLFLEHNGYRSLALGHISITEPEPSYDDDDYGYSEVLXAP 75
QY 37 KTSKRTMYDCTTEERAYSAEKCEPSSSE-----BENDVPSAATLNIPLEA 86
DB 76 SASKRTMYEDCEERKSAKSAKSSCDSSSPGYDENKTYLHNSNISEARLAI----- 131
QY 87 GNSWSEIFEL-----RKYVKNKGTSTIANKAWDSDHKLGCAYVDCSK-----THVY 136
DB 132 -LSMAEAFDLNKTGEGVLYRSLTISFNAILAMDTRKFGCAVACPLKDTSATTHVY 190
QY 137 CQYGPBANG--DGKTYEGAPCSRCSYD 163
DB 191 CHY-PRIEGEEREGKQIYKVGTPCGDCSEY 219

RESULT 3
US-08-450-497-86
; Sequence 86, Application US/08450497
; Patent No. 5919900
; GENERAL INFORMATION:
; APPLICANT: MATTHEW MOYLE, ET AL.
; TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,497
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/173,510
; FILING DATE: 23-DEC-1993
; APPLICATION NUMBER: 08/151,064
; FILING DATE: 10-NOV-1993
; APPLICATION NUMBER: 08/060,433
; FILING DATE: 11-MAY-1993
; APPLICATION NUMBER: 07/996,972
; FILING DATE: 24-DEC-1992
; APPLICATION NUMBER: 07/881,721
; FILING DATE: 11-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 205/073
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
US-08-450-497-86

Query Match 30.0%; Score 299; DB 2; Length 231;

Best Local Similarity 35.2%; Pred. No. 4.2e-25;
Matches 74; Conservative 20; Mismatches 58; Indels 58; Gaps 8;

QY 6 LCOORER-----LDDMKREFTELHNGYRAAFARNY-----K 37
DB 16 ICSNGMGNGFNDISRLKFLHNGYRSLALGHVISTEESEDDYLYLAA 96
QY 37 KTSKMTWYDCTLEKRAKSAKCESEPSSE-----ENVDSATLNIPLEA 87
DB 76 SASKMTWYDCTLEKRAKSAKCESEPSSE-----ENVDSATLNIPLEA 131
QY 87 GNSWSEITEL-----RGVYNKNGKTSNINANNVDSHDKLCAVYDCSGK-THVY 136
DB 132 -LSMAKAFDNLKTBGVLVRSNLITISNFANLMDTRKFCVAVAKCPKLDTSATTIHV 190
QY 137 COYGEPAK---DGTTEEGAPCSRCSDY 163
DB 191 CHY-PKIEGEKRGKQIYKGTGCGDCEX 219

RESULT 4

US-08-173-510B-84
Sequence 84, Application US/08173510B
Patent No. 5747296
GENERAL INFORMATION:
APPLICANT: MATTHEW MOYLE, ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,510B
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOV-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 205/073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
US-08-173-510B-84

Query Match 29.1%; Score 290.5; DB 1; Length 232;
Best Local Similarity 37.3%; Pred. No. 3.6e-24;
Matches 75; Conservative 23; Mismatches 60; Indels 43; Gaps 7;

QY 1 ESDYSLCOQREKT---DDMKREFTELHNGYRAAFARNY-----K 37
DB 37 EHDPTCPQNGEKMEKGFDAIRLKLFLAHNGYRSLALGHVISTEESEDDYLYLAA 96
QY 38 TSKMTWYDCTLEKRAKSAKCESEPSSE-----ENVDSATLNIPLEA 87
DB 97 ASKMTWYDCTLEKRAKSAKCESEPSSE-----ENVDSATLNIPLEA 151
QY 88 NWSWSEITEL-----RGVYNKNGKTSNINANNVDSHDKLCAVYDCSGK-THVY 142
DB 152 ISMAKAFDNLKTBGVLVRSNLITISNFANLMDTRKFCVAVAKCPKLDTSATTIHV 211
QY 143 AKDGKTYIEGAPCSRCSDY 163
DB 212 SRKKNPYYTGTGRCGCGSDY 232

RESULT 5

US-08-458-218-82
Sequence 82, Application US/08458218
Patent No. 5789178
GENERAL INFORMATION:
APPLICANT: MATTHEW MOYLE ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,218
FILING DATE: 24-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOVEMBER-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 203/226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
US-08-458-218-82

Query Match 29.1%; Score 290.5; DB 1; Length 232;
Best Local Similarity 37.3%; Pred. No. 3.6e-24;
Matches 75; Conservative 23; Mismatches 60; Indels 43; Gaps 7;

QY 1 EGDYSLCOQREKL-----DDMRMFTLHNGYRAAFARNY-----K 37
DB 37 EHPPTCPONGEMKRGPDDAIRLKFAMHNGYRSRLAGHVSITERSEDDYLDLYLAPR 96
QY 38 TSKRMVYDCTLEEKAYKSAEKCSEEPSSEB---ENV-----DVSAAATLNIPLAEG 87
DB 97 ASQMRILKDCDEAKRSAYESAKKCOYTASWEKRDENLQVIEDPKINHA-----LKAI 151
QY 88 NSWMSIEFL-----RGVYKNGKTSNLANVMDSHDKLCAVYDCSGK-THVYCOQYPE 142
DB 152 ISWATEAFNLKNGTEGGVYRSILDISNFRANLAMPTREKVCACAVKCSPTTHVYCHYPRK 211
QY 143 AKGDGKTYIEEGAPCSNCSY 163
DB 212 SRKRENPITYTGNRCGCSY 232

RESULT 6
US-08-450-497-84
Sequence 84, Application US/08450497
Patent No. 5919900
GENERAL INFORMATION:
APPLICANT: MATTHEW MOYLE, ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/173,510
FILING DATE: 23-DEC-1993
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOV-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 205/073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
US-08-450-497-84

Query Match 29.1%; Score 290.5; DB 2; Length 232;
Best Local Similarity 37.3%; Pred. No. 3.6e-24;
Matches 75; Conservative 23; Mismatches 60; Indels 43; Gaps 7;

QY 1 EGDYSLCOQREKL-----DDMRMFTLHNGYRAAFARNY-----K 37
DB 37 EHPPTCPONGEMKRGPDDAIRLKFAMHNGYRSRLAGHVSITERSEDDYLDLYLAPR 96
QY 38 TSKRMVYDCTLEEKAYKSAEKCSEEPSSEB---ENV-----DVSAAATLNIPLAEG 87
DB 97 ASQMRILKDCDEAKRSAYESAKKCOYTASWEKRDENLQVIEDPKINHA-----LKAI 151
QY 88 NSWMSIEFL-----RGVYKNGKTSNLANVMDSHDKLCAVYDCSGK-THVYCOQYPE 142
DB 152 ISWATEAFNLKNGTEGGVYRSILDISNFRANLAMPTREKVCACAVKCSPTTHVYCHYPRK 211
QY 143 AKGDGKTYIEEGAPCSNCSY 163
DB 212 SRKRENPITYTGNRCGCSY 232

RESULT 7
US-08-173-510B-83
Sequence 83, Application US/08173510B
Patent No. 5747296
GENERAL INFORMATION:
APPLICANT: MATTHEW MOYLE, ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,510B
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOV-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 205/073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
US-08-173-510B-83

Query Match 29.1%; Score 290; DB 1; Length 274;
Best Local Similarity 34.3%; Pred. No. 5.3e-24;
Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;

QY 51 EKKYYSARKCEE---PSEENEVDVSAATLII---PLEGNMWSSEITEL-----R 98
 Db 95 EKSYMSARNCDSSSPPEGIDENKIFENSN-NISEALKMISMKNKAFNLNTKEGE 153
 QY 99 GKYYNKGSTNSIAHWYWDHDKLCAVVD-----SGKT-----HYVCGAPE 142
 Db 154 GVLVRSNHDISNFMALMDAREKFGCAVYVNCPLGEIDETNHDSETATATTIHYVCHYKRI 2133
 QY 143 AKGDGKTIIEBAGPCSRCSY 163
 Db 214 NKIEGPIIKVGTPODDCSEY 234

RESULT 10
US-08-173-510B-87

1 GENERAL INFORMATION:
2 APPLICANT: MATTHEW MOYLE, ET AL.
3 TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
4 NUMBER OF SEQUENCES: 104
5 CORRESPONDENCE ADDRESS:
6 ADDRESSER: Lyon & Lyon
7 STREET: 633 West Fifth Street
8 STREET: Suite 4700
9 CITY: Los Angeles
10 STATE: California
11 COUNTRY: U.S.A.

```

? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5" Diskette, 1.44 MB
? MEDIUM TYPE: storage
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: IBM P.C. DOS 5.0
? SOFTWARE: Word Perfect 5.1
? COMMENTS:

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Query Match	26.7%;	Score 266;	DB 1;	Length 224;
Best Local Similarity	33.8%;	Pred. No. 1.8e-21;		
Matches 66;	Conservative 21;	Mismatches 56;	Indels 52;	Gaps 7;

Db 91 AEA^{SA}MS^{AR}NC^{SS}SS^{PE}PC^{EN}RY^{IE}NS^N-NISEA^{LK}AM^{IS}PA^{KE}FN^{IN}TEGE 149

QY 99 GK^YYN^{KG}TS^{IN}AN^WMS^{HD}KL^{CA}V^{YD}-----SGK^T-----HY^QY^{GP}E 142

Db 150 G^VY^{RS}N^{HD}IS^{FN}ML^{MD}RE^{FC}GA^VY^{NC}PL^{GE}ID^{GT}TH^{DE}Y^{AT}TI^{HY}CH^YPM 209

QY 143 AK^{GD}K^{TI}Y^{EG}AP^C 157

Db 210 NK^{TE}GP^{IT}K^YGR^{PC} 224

RESULT 11
US-08-458-218-85
; Sequence 85, Application US/08458218
; Patent No. 5789178

APPLICANT: MATTHEW MOYLE ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 102
CONFORMANCE ADDRESS: 102
CORRESPONDENCE ADDRESS: 102
STREET: 613 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: California
ZIP: U.S.A.
ZIP: 90071

```

1 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
2 MEDIUM TYPE: storage
3 COMPUTER: IBM Compatible
4 OPERATING SYSTEM: IBM P.C. DOS 5.0
5 SOFTWARE: Word Perfect 5.1
6 CURRENT APPLICATION DATA: 100,000,000

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Query Match	26.7%;	Score 266;	DB 1;	Length 224;
Best Local Similarity	33.8%;	Pred. No. 1.8e-21;		
Matches	66;	Conservative	21;	Mismatches 56;
			Indels	52;
			Gaps	7;

Db 347 ALMRPMOIGHYTMANDTYIKGAVNFCNFTFGVQIGPGNMGVITMOCPS 406
QY 159 RCDPYGAGYTC 169
Db 407 GCS---PGATC 414

RESULT 14

US-08-173-510B-85
; Sequence 85: Application US/08173510B
; Patent No. 5747266
; GENERAL INFORMATION:
; APPLICANT: MATTHEW MOYLE, ET AL.
; TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173, 510B
; FILING DATE: 23-DEC-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/151,064
; FILING DATE: 10-NOV-1993
; APPLICATION NUMBER: 08/060,433
; FILING DATE: 11-MAY-1993
; APPLICATION NUMBER: 07/996,972
; FILING DATE: 24-DEC-1992
; APPLICATION NUMBER: 07/881,721
; FILING DATE: 11-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 205/073
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ. ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
US-08-173-510B-85

Query Match 25.6%; Score 255; DB 1; Length 208;
Best Local Similarity 36.5%; Pred. No. 2,6e-20;
Matches 65; Conservative 18; Mismatches 55; Indels 40; Gaps 8;
QY 14 DDDREMEFTLHNGRYAPARNY--KTSKRTIYVDCITLKKAYKSAKC--SEPPSSE 68
Db 3 DDD-----YEGGLPDPFAPRASKRYLEYDCEAKSAVYASNSNSISPPGEGY 51
QY 69 EENDVFSATLNI--PLEAGNSWSEIFEL---RGKVYKNGKTSNIANNVWDSDHK 121
Db 52 DENKTIENSN-NISBAALKAMISMAKEAFNLNKTGEGVLYRSLNLTISNPNANLAWDTREK 110
QY 122 LGCAVVDGS-GK-----THVVCQYGPENKGDGKTIYEGAPCSRCSY 163
Db 111 FGCAVAVNCPGKRDALITDDEENYATAIHVYCHYPRINKTEGQPIYKVGTPCDDCSEY 168

RESULT 15

US-08-458-218-83
; Sequence 83: Application US/08458218
; Patent No. 5785178
; GENERAL INFORMATION:
; APPLICANT: MATTHEW MOYLE ET AL.
; TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,218
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/151,064
; FILING DATE: 10-NOVEMBER-1993
; APPLICATION NUMBER: 08/060,433
; FILING DATE: 11-MAY-1993
; APPLICATION NUMBER: 07/881,721
; FILING DATE: 11-MAY-1992
; APPLICATION NUMBER: 07/996,972
; FILING DATE: 24-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 203/226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ. ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
US-08-458-218-83

Query Match 25.6%; Score 255; DB 1; Length 208;
Best Local Similarity 36.5%; Pred. No. 2,6e-20;
Matches 65; Conservative 18; Mismatches 55; Indels 40; Gaps 8;
QY 14 DDDREMEFTLHNGRYAPARNY--KTSKRTIYVDCITLKKAYKSAKC--SEPPSSE 68
Db 3 DDD-----YEGGLPDPFAPRASKRYLEYDCEAKSAVYASNSNSISPPGEGY 51
QY 69 EENDVFSATLNI--PLEAGNSWSEIFEL---RGKVYKNGKTSNIANNVWDSDHK 121
Db 52 DENKTIENSN-NISBAALKAMISMAKEAFNLNKTGEGVLYRSLNLTISNPNANLAWDTREK 110
QY 122 LGCAVVDGS-GK-----THVVCQYGPENKGDGKTIYEGAPCSRCSY 163
Db 111 FGCAVAVNCPGKRDALITDDEENYATAIHVYCHYPRINKTEGQPIYKVGTPCDDCSEY 168
RESULT 16
US-08-450-497-85
; Sequence 85: Application US/08450497
; Patent No. 5919300

GENERAL INFORMATION:
APPLICANT: MATTHEW MOYLE, ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: California
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,497
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/173,510
FILING DATE: 23-DEC-1993
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOV-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 205/073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
US-08-450-497-85

Query Match 25.6%; Score 255; DB 2; Length 208;
Best Local Similarity 36.5%; Pred. No. 2.6e-20;
Matches 65; Conservative 18; Mismatches 55; Indels 40; Gaps 8;

QY 14.DDDAREFTELHNGYAAAFARNY--KTSKRTVYTCILEEKAYSAKRC---SEEPSSE 68
DB 3 DDD-----YKGLPDPAPRASKKMTLETCENAKSAIYASANCSTISPEEGY 51
QY 69.EENDVYSAATLNI---PLEAGNSWSEIPEL---RGKYYNKGKTSNTANAYWDSDHK 121
DB 52.DENKTIIEGNSN-NISPAALKAMISWAKENLNKGTGEGVLYRNSLTLSNFRANLAMDTRK 110

QY 122.LGCAVYDCS-GK-----THVYCOYGEPAKGDGKTYIEGAPCSRCSDY 163
DB 111.FGCAVYVNCPLGKPDALITIDDEENATATAHVYCHPRINTEGQPIYKVGTPCDDCSEY 168

RESULT 17
US-07-930-686-10
Sequence 10, Application US/07930686
Patent No. 5525508
GENERAL INFORMATION:
APPLICANT: Sharp, Phillip J
APPLICANT: Wagland, Barry M
APPLICANT: Cobon, Gary S

TITLE OF INVENTION: Nematode Vaccine
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley and Lardner
STREET: Suite 500, 1800 Diagonal Road
CITY: Alexandria
STATE: Virginia
COUNTRY: United States of America
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/930,686
FILING DATE: 19921006
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK4486
FILING DATE: 06-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00040
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A
REGISTRATION NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-930-686-10

Query Match 20.6%; Score 205; DB 1; Length 454;
Best Local Similarity 28.5%; Pred. No. 2.7e-14;
Matches 55; Conservative 36; Mismatches 74; Indels 28; Gaps 8;

QY 13.LDDMREMFTELHNGYAAAFARNY-----KTSKRTVYTCILEEKAYSAKCS 62
DB 262.MDEARKRFYVUKHNEYSLIAKGAKRGQFAPKARABMKVNYDCDVEANAMKSTCT 321
QY 63.EEPSSE-----ENDVYSAATLN---IPLEAGNSWSEIPEL---RGKYYNKGK-- 108
DB 322.FGINTRAALUKMGNNMAMSSKANKTEAAAEVAAVAFGDLKYGVPENNVFTYNYTTL 381
QY 109.SINAWYWDSDHKLGCAVYDC-SGKTHVYCOYGEPAKGDGKTYIEGAPCSRCSDYGA-G 166
DB 382.SKYSQAWSSDRIGCYVPCWSSWTVVCCERPNCGDLREALIDVGDPCTKADDCOCPE 441

QY 167.VYCDMDMNLICIT 179
DB 442.CTCSRD--EGLCV 452

RESULT 18
US-08-460-998-10
Sequence 10, Application US/08460998
Patent No. 5942413
GENERAL INFORMATION:
APPLICANT: Sharp, Phillip J
APPLICANT: Wagland, Barry M
APPLICANT: Cobon, Gary S
TITLE OF INVENTION: Nematode Vaccine
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley and Lardner
STREET: Suite 500, 3000 K Street, NW

```

CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/460,998
APPLICATION NUMBER: US/08/460,998
FILING DATE: 05-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/930,686
FILING DATE: 06-OCT-1992
PRIOR APPLICATION DATA: AU PK4486
APPLICATION NUMBER: AU PK4486
FILING DATE: 06-FEB-1991
PRIOR APPLICATION DATA: PCT/AU92/00040
APPLICATION NUMBER: PCT/AU92/00040
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A
REGISTRATION NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-460-998-10

Query Match      20.6%; Score 205; DB 2; Length 454;
Best Local Similarity 28.5%; Pred. No. 2.7e-14;
Matches 55; Conservative 36; Mismatches 74; Indels 28; Gaps 8;

OY 13 LDDNHEMTEHNGYRAAFARNY-----KTSKRTWYVYCT 62
DB 262 MTEAKRMEVDKHNHYSRLAKGAKRPGAPAPRAARMKVYDCDVAANMEMSKTC 321
OY 63 EEDSSEE-----ENVDFSAATLN---IPBAGSNWSEIFEL---RGKYNNKNGKT-- 108
DB 322 FGLNTAALMKRWGNMMSSKANNTTEAALAAVAWFGDLQKYGVPENNVFTMYVTTL 381
OY 109 SNIAANNVMSHDKLGCAVYDC-SGKTHVYCOYGPAPKDGKTIYEGAGCSCSPYGA-G 166
DB 382 SKYSQAMQSSDRICGYVPCWSTVYVCEYNPGDLPGEALTYDGDCTADQCPCG 441
OY 167 VTGDDDMQWLICI 179
DB 442 CTCNRD--EGLCV 452

RESULT 19
US-08-173-510B-89
; Sequence 89; Application US/08173510B
; Patent No. 5747296
; GENERAL INFORMATION:
; APPLICANT: MATTHEW MOYLE ET AL.
; TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,510B
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOV-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 205/073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
US-08-173-510B-89

Query Match      20.1%; Score 200; DB 1; Length 189;
Best Local Similarity 32.9%; Pred. No. 2.7e-14;
Matches 50; Conservative 16; Mismatches 46; Indels 40; Gaps 6;

OY 15 DDNHEMTEHNGYRAAFARNY-----KTSKRTWYVYCT 49
DB 40 DSIRLFLAMHNGYRSLALGHIGISKESIGDDYDDVYFYSVAPMAMSKRYLEYDCD 99
OY 50 LEEAVAKSEKSEE---PSEENVDF-SAAATLNIPLEGN---SNWSEIFEL----- 97
DB 100 SERAVYMSNSGSDSSPPEGYDENKNTILNSSNIN---EAARLAIIISGKRAFLNETG 156
OY 98 RGKYNNKNGKTSINANNVMSHDKLGCAVYDC 129
DB 157 EGYLVISNLTISFANLANMDTRREKFCAYVKC 188

RESULT 20
US-08-458-218-87
; Sequence 87; Application US/08458218
; Patent No. 5780178
; GENERAL INFORMATION:
; APPLICANT: MATTHEW MOYLE ET AL.
; TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
```


FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: AMINO ACIDS
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-930-686-12

Query Match 19.8%; Score 197.5; DB 1; Length 440;
Best Local Similarity 27.7%; Pred. No. 1.8e-13;
Matches 57; Conservative 35; Mismatches 77; Indels 37; Gaps 11;

DB 6 LCOQREK-LDDMREMTLHNGYRAAFARNY-----KTSKRTMYDCTLEKA 54
DB 238 MCPENNNGMTDEARQMFVDKNEHSLIKGLAHNNIGFAPFAAMKRVSYNCEIEANR 297
QY 55 YKAEKCEPSSSEEN---VDVFSAAAT-LNIPLEAGNS--WASE-----IFE 96
DB 298 VEMAKDCTLGYNVAQNNGQYVHSLPHINKTVAAESVEAMFELQTYGAPQDNVFS 357
QY 97 LRKRYNNKGTSTIANMVDSDHKLGCAYVDCSG--KTHVVCQYCPKAGDKGKTYIEEG 154
DB 358 M--EVENON-VIQEYLAOLAMQSSNOIGCIFSCWGAFTVACEYNGNFTIGELITMG 414
QY 155 APCSRCS-D-YGAGVTCDDDMQNLICI 179
DB 415 DPCSTDEDCQACGCVSKD--EALCI 438

RESULT 23
US-08-460-998-12
Sequence 12, Application US/08460998
Patent No. 5942413
GENERAL INFORMATION:
APPLICANT: Sharp, Phillip J
APPLICANT: Magland, Barry M
APPLICANT: Cobon, Gary S
TITLE OF INVENTION: Nematode Vaccine
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley and Lardner
STREET: suite 500, 3000 K Street, NW
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,998
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,686
FILING DATE: 06-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK4486
FILING DATE: 06-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00040
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A

REGISTRATION NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-460-998-12

Query Match 19.8%; Score 197.5; DB 2; Length 440;
Best Local Similarity 27.7%; Pred. No. 1.8e-13;
Matches 57; Conservative 35; Mismatches 77; Indels 37; Gaps 11;

QY 6 LCOQREK-LDDMREMTLHNGYRAAFARNY-----KTSKRTMYDCTLEKA 54
DB 238 MCPENNNGMTDEARQMFVDKNEHSLIKGLAHNNIGFAPFAAMKRVSYNCEIEANR 297
QY 55 YKAEKCEPSSSEEN---VDVFSAAAT-LNIPLEAGNS--WASE-----IFE 96
DB 298 VEMAKDCTLGYNVAQNNGQYVHSLPHINKTVAAESVEAMFELQTYGAPQDNVFS 357
QY 97 LRKRYNNKGTSTIANMVDSDHKLGCAYVDCSG--KTHVVCQYCPKAGDKGKTYIEEG 154
DB 358 M--EVENON-VIQEYLAOLAMQSSNOIGCIFSCWGAFTVACEYNGNFTIGELITMG 414
QY 155 APCSRCS-D-YGAGVTCDDDMQNLICI 179
DB 415 DPCSTDEDCQACGCVSKD--EALCI 438

RESULT 24
PCT-US96-07709-33
Sequence 33, Application PC/TUS9607709
GENERAL INFORMATION:
APPLICANT: Timp, Cynthia A.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Rose & McIntosh
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07709
FILING DATE: 23-MAY-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Cornell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-30-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-07709-33

Query Match 15.5%; Score 155; DB 5; Length 204;
Best Local Similarity 26.4%; Pred. No. 2.8e-09;
Matches 48; Conservative 24; Mismatches 68; Indels 42; Gaps 9;

QY 9 OREKIDDDMRMFTLHNGYRAAFARNT--KTSKMTWYDCTLEKAYSAEC--SEE 64
DB 12 ERKIVGQNNKRYSDLNGKLNKNGTYMPRGKMLDELWDCKLESSAQRVANOCIFGHS 71
QY 65 PSSEENV--DVF-----SAATLNIPLDAGNSMSEIFELRGVYNNKNGKTS 109
DB 72 PROGREVGENVYAYVSSVYEGLKKTAGT----DAGKSMWSEL---PLYENPNSNN 122
QY 110 -----NIANNWMSHDKLCAY-VDCSG--KTHVCOYGEPAKGDGKTIYEBA 155
DB 123 MTKVAGGVHLFTQAMNGKTYKICGVAATCCDGRLLIVICHYSPGGMVGEVIYORGN 182
QY 156 PC 157
DB 183 PC 184

RESULT 25
PCT-US96-07709-30
; Sequence 30, Application PC/TUS9607709
; GENERAL INFORMATION:
; APPLICANT: Tripp, Cynthia A.
; TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 23-MAY-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-30-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-07709-30

Query Match 15.5%; Score 155; DB 5; Length 220;
Best Local Similarity 26.4%; Pred. No. 3.2e-09;
Matches 48; Conservative 24; Mismatches 68; Indels 42; Gaps 9;

QY 9 OREKIDDDMRMFTLHNGYRAAFARNT--KTSKMTWYDCTLEKAYSAEC--SEE 64
DB 28 ERKIVGQNNKRYSDLNGKLNKNGTYMPRGKMLDELWDCKLESSAQRVANOCIFGHS 87
QY 65 PSSEENV--DVF-----SAATLNIPLDAGNSMSEIFELRGVYNNKNGKTS 109
DB 88 PROGREVGENVYAYVSSVYEGLKKTAGT----DAGKSMWSEL---PLYENPNSNN 138

QY 110 -----NIANNWMSHDKLCAY-VDCSG--KTHVCOYGEPAKGDGKTIYEBA 155
DB 139 MTKVAGGVHLFTQAMNGKTYKICGVAATCCDGRLLIVICHYSPGGMVGEVIYORGN 198
QY 156 PC 157
DB 199 PC 200

RESULT 26
PCT-US96-07709-25
; Sequence 25, Application PC/TUS9607709
; GENERAL INFORMATION:
; APPLICANT: Tripp, Cynthia A.
; TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 23-MAY-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-30-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-07709-25

Query Match 15.5%; Score 155; DB 5; Length 248;
Best Local Similarity 26.4%; Pred. No. 3.8e-09;
Matches 48; Conservative 24; Mismatches 68; Indels 42; Gaps 9;

QY 9 OREKIDDDMRMFTLHNGYRAAFARNT--KTSKMTWYDCTLEKAYSAEC--SEE 64
DB 56 ERKIVGQNNKRYSDLNGKLNKNGTYMPRGKMLDELWDCKLESSAQRVANOCIFGHS 115
QY 65 PSSEENV--DVF-----SAATLNIPLDAGNSMSEIFELRGVYNNKNGKTS 109
DB 116 PROGREVGENVYAYVSSVYEGLKKTAGT----DAGKSMWSEL---PLYENPNSNN 166
QY 110 -----NIANNWMSHDKLCAY-VDCSG--KTHVCOYGEPAKGDGKTIYEBA 155
DB 167 MTKVAGGVHLFTQAMNGKTYKICGVAATCCDGRLLIVICHYSPGGMVGEVIYORGN 226
QY 156 PC 157
DB 227 PC 228

RESULT 27
US-08-773-368-1

Page 14

```

      TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED  

      TITLE OF INVENTION: PROTEIN  

      NUMBER OF SEQUENCES: 6  

      CORRESPONDENCE ADDRESS:  

      ADDRESSEE: Incyte Pharmaceuticals, Inc.  

      STREET: 3174 Porter Drive  

      CITY: Palo Alto  

      STATE: CA  

      COUNTRY: USA  

      ZIP: 94304  

      COMPUTER READABLE FORM:  

      MEDIUM TYPE: Diskette  

      COMPUTER: IBM Compatible  

      OPERATING SYSTEM: DOS  

      SOFTWARE: FASTSEQ for Windows Version 2.0  

      CURRENT APPLICATION DATA:  

      APPLICATION NUMBER: US/09/199,887  

      FILING DATE:  

      CLASSIFICATION:  

      PRIOR APPLICATION DATA:  

      APPLICATION NUMBER: 08/773,368  

      FILING DATE:  

      ATTORNEY/AGENT INFORMATION:  

      NAME: Billings, Lucy RJ  

      REGISTRATION NUMBER: 36,749  

      REFERENCE/DOCKET NUMBER: PF-0186 US  

      TELECOMMUNICATION INFORMATION:  

      TELEPHONE: 415-855-0555  

      TELEFAX: 415-845-4166  

      TELEX:  

      INFORMATION FOR SEQ ID NO: 1:  

      SEQUENCE CHARACTERISTICS:  

      LENGTH: 270 amino acids  

      TYPE: amino acid  

      STRANDEDNESS: single  

      TOPOLOGY: linear  

      IMMEDIATE SOURCE:  

      CLONE: 1393164  

      US-09-199-887-1  

  

      Query Match          15.1%; Score 151; DB 3; Length 270;  

      Best Local Similarity 28.6%; Pred. No. 1.2e+08;  

      Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 10;  

  

      Db              13 LDDDEREFTELNGYRAAFARNTKTSKRRTVYDCITL--EKAYISAENC--SEPSSE 68  

      QY              1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  

      Db              28 LTDEEKRMLWELNHLRAOVSPF--ASDYLHHRMDEELAAFAAKAAROXRGXHNKKRGR 85  

      QY              1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  

      Db              69 EENVAVFPAALNIPILEAGNSMWSEIFELRGVYNKNKGATSNIAIM-----VMSHDK 121  

      QY              1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  

      Db              86 GEHTLAITDEGMVPL-AAMEWHNE-----REHYNLNAATCSFGOMCHYTQVMMAKTER 139  

      QY              1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  

      Db              122 ICAAVVDS-----GTHY--VCQYGPEAKGDGTIIEBGAPCSRCSIDYAGATCDDDM 173  

      QY              1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  

      Db              140 IGGSHPECRIQGVETIELLYCNTPGNAVKGRRPYCGTFCSCCP---SGVHC---- 192  

      QY              1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  

      Db              174 ONLLC 178  

      QY              1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  

      Db              193 KNSLC 197  

  

      RESULT 29  

      US-08-173-510B-88  

      Sequence 88; Application US/08173510B  

      Patent No. 5747236  

      GENERAL INFORMATION:  

      APPLICANT: MATTHEW MOYLE, ET AL.  

      TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS  

      NUMBER OF SEQUENCES: 104  

      CORRESPONDENCE ADDRESS:  

      ADDRESSEE: Lyon & Lyon  

      STREET: 633 West Fifth Street  

      STREET: Suite 4700
    
```

CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,510B
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOV-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 205/073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
US-08-173-510B-88

Query Match 14.4%; Score 144; DB 1; Length 146;
Best Local Similarity 33.6%; Pred. No. 2.8e-08;
Matches 40; Conservative 13; Mismatches 32; Indels 34; Gaps 4;

QY 8 GOREKLDMDREMFTELHNGYRAAFARNY-----KTSKMTWYDC 48
DB 30 EMEKGFDDAMRLKFLAHNGYRSLALGHVSITESESDYDLYDSYAPTASKMYRLKYDC 89
QY 49 TLEEKAYSAKCESEPSSE---EENV-----DVSAAATLNIPLGNSWMSSEIFEL 97
DB 90 EMEKATYSARKCQTTSSTKYDENLVQVIEDPRDINHAA-----LKNATISMAEAFNL 143

RESULT 30
US-08-458-218-86
Sequence 86; Application US/08458218
Patent No. 5789178
GENERAL INFORMATION:
APPLICANT: MATTHEW MOYLE ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,218
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOVEMBER-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 203/226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
US-08-458-218-86

Query Match 14.4%; Score 144; DB 1; Length 146;
Best Local Similarity 33.6%; Pred. No. 2.8e-08;
Matches 40; Conservative 13; Mismatches 32; Indels 34; Gaps 4;

QY 8 GOREKLDMDREMFTELHNGYRAAFARNY-----KTSKMTWYDC 48
DB 30 EMEKGFDDAMRLKFLAHNGYRSLALGHVSITESESDYDLYDSYAPTASKMYRLKYDC 89
QY 49 TLEEKAYSAKCESEPSSE---EENV-----DVSAAATLNIPLGNSWMSSEIFEL 97
DB 90 EMEKATYSARKCQTTSSTKYDENLVQVIEDPRDINHAA-----LKNATISMAEAFNL 143

RESULT 31
US-08-450-497-88
Sequence 89; Application US/08450497
Patent No. 5919800
GENERAL INFORMATION:
APPLICANT: MATTHEW MOYLE ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,497
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/173,510
FILING DATE: 23-DEC-1993
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOV-1993
APPLICATION NUMBER: 08/060,433

FILED DATE: 11-MAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 205/073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3511
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
US-08-450-944-5

Query Match 14.4%, Score 144; DB 2; Length 146;
Best Local Similarity 33.6%, Pred. No. 2,8e-08;
Matches 40; Conservative 13; Mismatches 32; Indels 34; Gaps 4;

QY 8 QQREKIDDMREMTLHNGYRAAFARNY-----KTSKRTMYDC 48
DB 30 EMKGFDDMRKLTALHNGYRSLALGHVSTTESEEDYLDLSYAPASMRKLYDC 89
QY 49 TLEKAKSAEKSEEPSE---ENVY-----DVFSATLNIPLDAGNSWMSSEIFEL 97
DB 90 EAKSAVESAKKCOQTASSSTKYDENLQVIEDPRDINHAA-----LKATISWATEAFVL 143

RESULT 32
US-08-450-944-5
Sequence 5, Application US/08450944
Patent No. 5789194
GENERAL INFORMATION:
APPLICANT: Trilip, Cynthia A.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: PARASTIC HELMINTH VENOM ALLERGEN
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,944
FILING DATE: 23-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2618-30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-5700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-450-944-5
Query Match 14.1%, Score 141; DB 1; Length 205;
Best Local Similarity 27.0%, Pred. No. 1e-07;
Matches 57; Conservative 17; Mismatches 65; Indels 72; Gaps 12;

QY 7 CQREKIDDMREMTLHNGYRAAFARNY-----KTSKRTMYDCLEKAYK 56
DB 3 CEGKLTPTTKRNITVOT-NKYSRLIRGLKLNKQGYLMPGKNMLRMKRDCKLEKSAON 61
QY 57 SAECG--SEPPSE---ENVYF-----SAATLNIPLDAGNSWMSSEIFELRG 99
DB 62 WAKCYFGHSPSESRGGEVYAVMSGSDVLDKKTAGT-----DAGRLMSEL-----E 112
QY 100 KTVR--KNGKTSNTA-----NMYWSDHKLCAVYDCSGKTH-----VYCO 138
DB 113 KYSDFNSNLTSEVAMENILHFTOMAGETRYKLD-----SGVDHVIYAVARTLVFICH 166
QY 139 YGPEAKGDKTYEGAPC-----SRCS 161
DB 167 YFPGNKNVADLTIELGNPCKHNDCKTRKCS 197

RESULT 33
PCT-US96-07709-5
Sequence 5, Application PC/TUS9607709
GENERAL INFORMATION:
APPLICANT: Trilip, Cynthia A.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: PARASTIC HELMINTH VENOM ALLERGEN
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07709
FILING DATE: 23-MAY-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-30-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-07709-5

Query Match 14.1%, Score 141; DB 5; Length 205;
Best Local Similarity 27.0%, Pred. No. 1e-07;
Matches 57; Conservative 17; Mismatches 65; Indels 72; Gaps 12;

QY 7 CQREKIDDMREMTLHNGYRAAFARNY-----KTSKRTMYDCLEKAYK 56
DB 3 CEGKLTPTTKRNITVOT-NKYSRLIRGLKLNKQGYLMPGKNMLRMKRDCKLEKSAON 61
QY 57 SAECG--SEPPSE---ENVYF-----SAATLNIPLDAGNSWMSSEIFELRG 99

DB 62 WANNVCVGHSPSSSRGIGENYAYWSSGSYRLDKTACT-----DAGRIMNSL-----E 112
QY 100 KYVN---KNGKTSNTA-----NMWDSHDLGCAVYDCSGKTH-----VYCO 138
DB 113 KYISDNSSNNLISEVAMENILHFTOMAMGETYKLG-----SGVDHNIYVARTLVFICH 166
QY 139 YGPEAKDGKTYIEGAPC-----SRCS 161
DB 167 YFGGNNYKDLITELGNPCKHNKDCRTKCS 197

RESULT 34
US-08-450-944-2
Sequence 2, Application US/08450944
Patent No. 5789194
GENERAL INFORMATION:
APPLICANT: TIPP, Cynthia A.
APPLICANT: Misnewski, Nancy
TITLE OF INVENTION: PARASTIC HELMINTH VENOM ALLERGEN
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,944
FILING DATE: 23-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Veseer, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2618-30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-9700
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 221 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-450-944-2

Query Match 14.1%; Score 141; DB 1; Length 221;
Best Local Similarity 27.0%; Pred. No. 1,1e-07;
Matches 57; Conservative 17; Mismatches 65; Indels 72; Gaps 12;

DB 7 COOREKLDMDREMTFLHNGYRAAFARNY-----KTSKRTMYVDCLEKAYK 56
QY 19 CEGGKLTPTERKNIVYQI-NKYRSRLRGKLNKDGILMPKGNMLRHRDCKLEKSAQN 77
DB 57 SAERC--SEBPSSE-----ENVDF-----SAATLNIPLFEGNSWSEIFELNG 99
QY 78 WANNVCVGHSPSSSRGIGENYAYWSSGSYRLDKTACT-----DAGRIMNSL-----E 128
DB 100 KYVN---KNGKTSNTA-----NMWDSHDLGCAVYDCSGKTH-----VYCO 138
QY 129 KYISDNSSNNLISEVAMENILHFTOMAMGETYKLG-----SGVDHNIYVARTLVFICH 182
DB 139 YGPEAKDGKTYIEGAPC-----SRCS 161
QY 167 YFGGNNYKDLITELGNPCKHNKDCRTKCS 213

RESULT 35
PCT-US96-07709-2
Sequence 2, Application PC/US9607709
Patent No. 5789194
GENERAL INFORMATION:
APPLICANT: TIPP, Cynthia A.
APPLICANT: Misnewski, Nancy
TITLE OF INVENTION: PARASTIC HELMINTH VENOM ALLERGEN
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07709
FILING DATE: 23-MAY-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-30-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 221 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-07709-2

Query Match 14.1%; Score 141; DB 5; Length 221;
Best Local Similarity 27.0%; Pred. No. 1,1e-07;
Matches 57; Conservative 17; Mismatches 65; Indels 72; Gaps 12;

DB 7 COOREKLDMDREMTFLHNGYRAAFARNY-----KTSKRTMYVDCLEKAYK 56
QY 19 CEGGKLTPTERKNIVYQI-NKYRSRLRGKLNKDGILMPKGNMLRHRDCKLEKSAQN 77
DB 57 SAERC--SEBPSSE-----ENVDF-----SAATLNIPLFEGNSWSEIFELNG 99
QY 78 WANNVCVGHSPSSSRGIGENYAYWSSGSYRLDKTACT-----DAGRIMNSL-----E 128
DB 100 KYVN---KNGKTSNTA-----NMWDSHDLGCAVYDCSGKTH-----VYCO 138
QY 129 KYISDNSSNNLISEVAMENILHFTOMAMGETYKLG-----SGVDHNIYVARTLVFICH 182
DB 139 YGPEAKDGKTYIEGAPC-----SRCS 161
QY 167 YFGGNNYKDLITELGNPCKHNKDCRTKCS 213

RESULT 36
US-07-857-224B-112
Sequence 112, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
CITY: Zurich

STATE: none
COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (international) 41 1 632 2830
TELEFAX: (international) 41 1 262 2437
TELEX: none
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 138
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
ORIGINAL SOURCE: human
ORGANISM: human
FEATURE: Testis specific protein; Table 17 Row 8
PUBLICATION INFORMATION:
AUTHORS:
AUTHORS: Kaahara, M.
AUTHORS: Gultnecht, J.
AUTHORS: Brew, K.
AUTHORS: Spurr, N.
AUTHORS: Goodfellow, P. N.
TITLE: Cloning and mapping of a testis-specific gene with sequence
TITLE: similarity to a sperm coating glycoprotein gene
JOURNAL: Genomics
VOLUME: 5
PAGES: 527-534
DATE: 1989
US-07-857-224B-112

Query Match 12.7%; Score 127; DB 2; Length 138;
Best Local Similarity 26.9%; Pred. No. 26-06;
Matches 39; Conservative 23; Mismatches 45; Indels 38; Gaps 8;

QY 38 TSKRMVYDCTLEE---KAYSAEKSE-----EPSEENVDFSAATLNIPLEGN 88
DB 10 TNAQRMARKCTLQSPEDRKSTRGENTLYMSDPTS-----MSAI-----Q 54

QY 89 SMMSEIFELRGKYNNKNGKTSN-----IANWYDSHDKLGAVYDC---SGKTHVCOY 139
DB 55 SMTDEILDF---YGVGPKSPNAVGHYQLWVSTYGVGGIAYCPNDLSKYYVCOY 111

QY 140 GPEAKGDGK--TIYEGAPCSRCD 162
DB 112 CPGNNMNRKNTPYQGTPCAGCPD 136

RESULT 37
US-08-773-368-4
Sequence 4, Application US/08773368
Patent No. 5856130
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Sura K.
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq for Windows version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/773,368
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy R.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0186 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 266 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1030053
US-08-773-368-4

Query Match 12.2%; Score 122; DB 2; Length 266;
Best Local Similarity 24.9%; Pred. No. 1.9e-05;
Matches 49; Conservative 30; Mismatches 68; Indels 50; Gaps 11;

QY 14 DDDREMFTELHNGRAFAARNYTSKRMVYDCTLEEKAYSAECS-----EPP- 65
DB 30 NEDFIKDCVRIHNRKSRVKPT--ASDMLYMTWDPALQIAKAWASNCQFSHTRLKPPH 87

QY 66 -----SSEEN-----VDVFSATLNIPLEGNMMSSEI--FELRKYNNKNGKTSNIA 112
DB 88 KLHNFSTLGENIWTGVSPIRVS-----AITWYDEIDYDFKTRICK--VCGHYT 139

QY 113 NMWYDSHDKLGAVYDC-----SGKTHVCOYGPEAKGDGKT--IYEGAPCSRCD 162
DB 140 QVWADSVYKGCAGVQFCPKVSGFDALSNNGAHFICNYGP--GNYPTWPKYRGATCSACP 197

QY 163 YGAGVTCDDDMONILCI 179
DB 198 -----NDKCLDNLCV 207

RESULT 38
US-09-199-887-4
Sequence 4, Application US/09199887
Patent No. 6071674
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Sura K.
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/09/199,887
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/773,368
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy RJ
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0186 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 266 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1030053
US-09-199-887-4

Query Match 12.2%; Score 122; DB 3; Length 266;
Best Local Similarity 24.9%; Pred. No. 1.9e-05;
Matches 49; Conservative 30; Mismatches 68; Indels 50; Gaps 11;

QY 14 DDDREFFTELHNGYRAAFARANYKTSKMTVYDCITLEEKAYKSAECS-----EEP- 65
DB 30 NEDFIKDCVRIHNRKFRSEVKPT--ASDMLYWTWDPALAIKAMVSNQCFSHNTRLKP 87
QY 66 -----SSEEN-----VDVFSATLNIPILEAGSNWSEIFELRCKYNNKNGKTSNAN 112
DB 88 KLHNFSTLSEGNITWTSVPILFVS-----ATNMWYDEIDQYKFRICK--VCGHT 139
QY 113 NMVDSHDKLGCAVYDC-----SGKTHVVCQYGPARGDGT--IYESGAPSCRS 162
DB 140 QVWADSYKVGCAVQFCPKVSGFDALNSGAHFICNTGP--GGNPTPTPKRGATCSACP 197
QY 163 YGAGVTCDDDMONLCI 179
DB 198 -----NDKCIDNLCV 207

RESULT 39
US-08-773-368-3
Sequence 3, Application US/08773368
Patent No. 5856130
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/09/199,887
FILING DATE:
CLASSIFICATION:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/773,368
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy RJ
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0186 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 847722
US-08-773-368-3

Query Match 12.1%; Score 121; DB 2; Length 219;
Best Local Similarity 25.1%; Pred. No. 1.8e-05;
Matches 49; Conservative 26; Mismatches 74; Indels 46; Gaps 9;

QY 14 DDDREFFTELHNGYRAAFARANYKTSKMTVYDCITLEEKAYKSAECS-----EEP- 65
DB 20 NEDFIKDCVRIHNRKFRSEVKPT--ASDMLYWTWDPALAIKAMVSNQCFSHNTRLKP 77
QY 66 -----SSEEN-----VDVFSATLNIPILEAGSNWSEIFELRCKYNNKNGKTSNAN 114
DB 78 KLHNFSTLSEGNITWTSVPILFVS-----ATNMWYDEIDQYKFRICK--VCGHT 131
QY 115 NMVDSHDKLGCAVYDC-----SGKTHVVCQYGPARGDGT--IYESGAPSCRS 164
DB 132 QVWADSYKVGCAVQFCPKVSGFDALNSGAHFICNTGP--GGNPTPTPKRGATCSACP 187
QY 165 AGVTCDDDMONLCI 179
DB 188 -----NDKCIDNLCV 197

RESULT 40
US-09-199-887-3
Sequence 3, Application US/09199887
Patent No. 6071874
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/09/199,887
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/773,368
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy KJ
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0186 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 847722
US-09-199-887-3

Query Match 12.1%; Score 121; DB 3; Length 219;
Best Local Similarity 25.1%; Pred. No. 1.8e-05;
Matches 49; Conservative 26; Mismatches 74; Indels 46; Gaps 9;

QY 14 DDDRMETELHNGRAAFARNTKMTWYDCTLEKAYSAKCS-----EEP- 65
DB 20 NEDFIDCVRIHNRFRSEVKPT--ASDMLYMTWDPALAQIKAMASNCQFSHTRLKPPH 77
QY 66 -----SSEEN-----VDVFSATNTINPLEAGNSMSEIFEELRGVYKKNKTSINAM 114
DB 78 KLHPNTSGENINWTSVPIFSVS-----AITWYDEIDQNFRTICKKVCCHYQV 131
QY 115 VMDSHKLCAVAVDC-----SGKTHVCOYGPFAKGGGT--TYEGAGCSCSDYG 164
DB 132 VMADSKYVCAVOFCPKVSGFDALSNAGHFICTGTP--GNYPTWPKKATCSACP-- 187
QY 165 AGVTCDDDMQNLICI 179
DB 188 ----NDKCLDMLCY 197

RESULT 41
US-07-857-224B-111
Sequence 111, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Bennett, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Bennett
STREET: Hadlaubstrasse 151
CITY: Zurich
STATE: none
COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION INFORMATION:
TELECOMMUNICATION INFORMATION: 41 1 632 2830
TELEPHONE: (International) 41 1 262 2437
TELEFAX: (International) 41 1 262 2437
TELEX: none
INFORMATION FOR SEQ ID NO: 111:

SEQUENCE CHARACTERISTICS:
LENGTH: 137
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: human
FEATURE: testis specific protein; Table 17 Row 7
PUBLICATION INFORMATION:
AUTHORS:
AUTHORS: Kasahara, M.
AUTHORS: Gutknecht, J.
AUTHORS: Brew, K.
AUTHORS: Spurr, N.
AUTHORS: Goodfellow, P. N.
TITLE: Cloning and mapping of a testis-specific gene with sequence
TITLE: similarity to a sperm coating glycoprotein gene
JOURNAL: Genomics
VOLUME: 5
PAGES: 527-534
DATE: 1989
US-07-857-224B-111

Query Match 11.5%; Score 115; DB 2; Length 137;
Best Local Similarity 28.0%; Pred. No. 4.2e-05;
Matches 35; Conservative 19; Mismatches 49; Indels 22; Gaps 6;

QY 54 AYKAERKSEPSSEENVDFSAATINPLEAGNSMSEIFEELRGVYKKN-----G 106
DB 13 AQKANKCNLEHSSDDR-KINIRGENTLWSTPTLWSTYIQ---SWYNEDDFYVG 68
QY 107 KTSIA-----NMVDSHDKLCAVAVDCSGKTHV---VCOYGEAGGDK--TYEEGA 155
DB 69 AKPNSAVGHYQIVYSSFKIGCIACVPMQDLKRYFYVCHYCPMGNVKKSTPYQGT 128
QY 156 PCSRC 160
DB 129 PCASC 133

RESULT 42
US-08-614-935-5
Sequence 5, Application US/08614935
Patent No. 5804201
GENERAL INFORMATION:
APPLICANT: King, Te P.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,935
FILING DATE: 11-MAR-1996
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-156
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800

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? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? HYPOTHEITICAL: NO
? ANTI-SENSE: NO
? FRAGMENT TYPE:
? ORIGINAL SOURCE:
? ORGANISM: Dolichovespula maculata
US-09-130-287-5

Query Match 11.3%; Score 112.5; DB 3; Length 204;
Best Local Similarity 23.4%; Pseq. No 0.00014;
Matches 33; Conservative 27; Mismatches 74; Indels 27; Gaps 6;

OY 13 LDDDKREFETLNGRAAFARANKT-----SKRTMYDCTLEAKYSAKRC- 61
DB 36 LINDENKELLNRHDDRONVAGLETRGRCGPQPPAKKNVYLVNDELAKIAQNRHQCQD 95
OY 62 -----SEEPSSEENVDS--AATNLPIEACNSWSSEIFELRGVYKNG--KTS 109
DB 96 FHHDDORTARYQVGGNINISSTATQFDPERKLKKQWEDVEEYFRYKAGQNSNPRKVG 155
OY 110 NNANVWDSHDKLCA--VYDCSGKTH-VQVOYSPKAGDGKTYE 152
DB 156 HYQWYMGKTRKIGCGSIXIEDWYHYLVQVYGPGRNDPNOPIYE 202

RESULT 44
US-08-614-935-4
Sequence 4, Application US/08614935
Patent No. 5804201
GENERAL INFORMATION:
APPLICANT: KING, Te P.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
TITLE OF INVENTION: ANTIGEN 5
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614.935
FILING DATE: 11-MAR-1996
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION/DOCKET NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEITICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Dolichovespula maculata
US-08-614-935-4

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Oy      14 DDDREMPTELLHNGVFAAPARYN-----KTSKARTVWYDCTL 50
      Oy      35 NDSIRLOPLAHHNGYSKSLALGHISTEESBDDDDDFGCLPDPAPARSKRYLEYDCEA 94
      Db      51 EEKAVKSKSEKSESE--PSESEENVDFSAATLNI--PLEAGNSWMSIEFL-----R 98
      Oy      95 ESKAVYSARNCSDBSSPPGCGYDENKTYFENSN-NISEALKAMISMAKEAENLNKTRKEE 153
      Db      99 GRYKNNKNTSIANNVWMSHDKIGCAVYDC-----SGKT-----HYVCOGPE 142
      Oy      154 GVLVYSNHDISNFPANLAWDAREKGCAGVYVNCPLGEIDETNNHDEGTATYTHVYCHPRKI 213
      Db      143 AKGDGKTYEGAGRCRSGDY 163
      Oy      214 NKTEGQPIYKVGTPCDDCSEY 234
      Db

RESULT 4
US-09-797-410-2
Sequence 2, Application US/09797410
Patent No. US2002009183A1
GENERAL INFORMATION:
APPLICANT: PluschkeU, Stefanie B.
APPLICANT: Geldart, Roderrick W.
APPLICANT: Ho, Lewis
APPLICANT: Koehlet, Mark A.
APPLICANT: Okehladi, Gary A.
APPLICANT: Plas, Steven J.
APPLICANT: Zhu, Marie M.
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF NEUTROPHIL INHIBITORY
FILE REFERENCE: SUZANNE L. BIGGS: CORVAS 259/001
CURRENT APPLICATION NUMBER: US/09/797,410
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 274
TYPE: PRT
ORGANISM: Ancylostoma caninum
US-09-797-410-2

Query Match      29.1%; Score 290; DB 10; Length 274;
Best Local Similarity 34.3%; Pred. No. 4,7e-21;
Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;

Oy      14 DDDREMPTELLHNGVFAAPARYN-----KTSKARTVWYDCTL 50
      Oy      35 NDSIRLOPLAHHNGYSKSLALGHISTEESBDDDDDFGCLPDPAPARSKRYLEYDCEA 94
      Db      51 EEKAVKSKSEKSESE--PSESEENVDFSAATLNI--PLEAGNSWMSIEFL-----R 98
      Oy      95 ESKAVYSARNCSDBSSPPGCGYDENKTYFENSN-NISEALKAMISMAKEAENLNKTRKEE 153
      Db      99 GRYKNNKNTSIANNVWMSHDKIGCAVYDC-----SGKT-----HYVCOGPE 142
      Oy      154 GVLVYSNHDISNFPANLAWDAREKGCAGVYVNCPLGEIDETNNHDEGTATYTHVYCHPRKI 213
      Db      143 AKGDGKTYEGAGRCRSGDY 163
      Oy      214 NKTEGQPIYKVGTPCDDCSEY 234
      Db

RESULT 5
US-10-051-644B-6
Sequence 6, Application US/10051644B
Patent No. US20030126625A1
GENERAL INFORMATION:
APPLICANT: Liu, et al.
TITLE OF INVENTION: Screens and Assays for Agents Useful in Controlling
FILE REFERENCE: 2002630-0012

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CURRENT APPLICATION NUMBER: US/10/051,644B
CURRENT FILING DATE: 2003-03-04
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 205
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Cluseta1 w
OTHER INFORMATION: Alignment of VAP-1, VAP-2, and selected other
US-10-051-644B-6

Query Match
Best Local Similarity 25.68; Score 255; DB 9; Length 205;
Matches 62; Conservative 27; Mismatches 70; Indels 32; Gaps 7;

QY 7 CQOREKIDDDREMEFTELHNGYRAAFARNY-----KTSKRTVYDCTLEEKAYK 56
DB 9 CPSNTGMDSVRDTFL-VHNEFRSSVANGLEPPDAGSNAPKAKMKKMYDCEVEASAIR 67
QY 57 SAERCSSEPSSEEE---NVDFSAATLNI-----PLEGNSMSEIFE-----LKG 99
DB 66 HCNKCYVOHSHGEDRGLGENTIKTSYKEDKKNAAKQASQLMWNELEKFGVGSNYLT 127
QY 100 KYTNKNG-KTSNINANNVWDSDHKLGCAYVDCSGKTHVYCGYGPPEAGDKTIYEEGAPCS 158
DB 128 ALMNPQMGIQHYTOMAMDTYKLGCAVAFECNPFEGVCGYGPNGMYGHVITYTMGSPCS 187
QY 159 RCDSDYGAGVTC 169
DB 188 QCS---PGATC 195

RESULT 6
US-10-051-644B-3
Sequence 3, Application US/10051644B
Publication No. US20030126625A1
GENERAL INFORMATION:
APPLICANT: Liu, et al.
TITLE OF INVENTION: Screens and Assays for Agents Useful in Controlling
FILE REFERENCE: 2002630-0012
CURRENT APPLICATION NUMBER: US/10/051,644B
CURRENT FILING DATE: 2003-03-04
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 473
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: VAP-2 Amino
US-10-051-644B-3

Query Match
Best Local Similarity 21.08; Score 209.5; DB 9; Length 473;
Matches 59; Conservative 26; Mismatches 87; Indels 45; Gaps 7;

QY 6 LCOOREKIDDD-----KMEFTELHNGYRAAFARNY-----KTSK 40
DB 256 LCAAPSMVYDDGSGCQCNLSVYTINFTLEQHNTSRLLKGFENWGETNTSOPKASQ 315
QY 41 MKRYVDTCTLEEKAYKSEK-----SEPPSSEENVDFSAAT---LNIPLGNSMW 91
DB 316 MKEKIDCTLEERAPQNNANNCVFNHSAHERPQGNQNTYMSFSNPDRSLHTNAEKW 375
QY 92 SEIFE-----LNGKYTNKNGT-SNINANNVWDSDHKLGCAYVDCSGKTHVYCGYGP 142
DB 376 QELEREGTPIDNLVLPPELMDLKGALGHYTOAMADRTYRLCGICANCPKMSYVCHYGP 435
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QY 143 AKGDGKTIYEEGAPCSRCSRDYAGVTCDDDMQNLICI 179
DB 436 GNRRNKKIYIEDDPCDEVDDCPIDGDCER--TTSICV 470

RESULT 7
US-10-051-644B-1
Sequence 1, Application US/10051644B
Publication No. US20030126625A1
GENERAL INFORMATION:
APPLICANT: Liu, et al.
TITLE OF INVENTION: Screens and Assays for Agents Useful in Controlling
FILE REFERENCE: 2002630-0012
CURRENT APPLICATION NUMBER: US/10/051,644B
CURRENT FILING DATE: 2003-03-04
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 425
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: VAP-1 Amino
US-10-051-644B-1

Query Match
Best Local Similarity 19.18; Score 190; DB 9; Length 425;
Matches 45; Conservative 40; Mismatches 79; Indels 32; Gaps 5;

QY 4 YSLCOOREKIDDDREMEFTELHNGYRAAFARNYKTSK-----RTMYDCTL 50
DB 222 FTWCPSTYDQSDQARQNFLDTHNKLKTSILAKGLDAGIAGAPAPAKOMPRFLVKISCTV 281
QY 51 EERKAYSARCSSEPSSEEE---NVDFSAATLNIPL-----EAGNSMSEIFE----- 96
DB 282 ENAKRTAKGLYHSTSAQRPELGENTLMTISINNMFKRTIARDSSKAWMSLDPFGVS 341
QY 97 ---LNGKYTNKNGT-SNINANNVWDSDHKLGCAYVDCSGKTHVYCGYGPENAGDKTIYEE 153
DB 342 DNLITQAVFDG--VGHYTOAMWEGTTEIGCEVENCPTFYSCGYGPAGNYMQLIYTK 399
QY 154 GAPCSRCSRDYAGVTC 169
DB 400 GSPECTRADDCPGTQTC 415

RESULT 8
US-09-808-602-27
Sequence 27, Application US/09808602
Patent No. US2002015115A1
GENERAL INFORMATION:
APPLICANT: Vernet, Corine A
APPLICANT: Fernandes, Elma
APPLICANT: Shinkels, Richard A
APPLICANT: Herzman, John L
APPLICANT: Majumder, Kundu
APPLICANT: Mishra, Vishnu
APPLICANT: Mezes, Peter S
APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US2002015115A1el Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-697 CIP
CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 300
```

TYPE: PRT
ORGANISM: Homo sapiens
US-09-808-602-27

Query Match 15.0% Score 160; DB 9; Length 300;
Best Local Similarity 25.5% Pred No 5.3e-08;
Matches 53; Conservative 31; Mismatches 66; Indels 58; Gaps 11;

QY 1 EGDYSLCOOREK---LDDMEKMEFELHNGYRAAFARNTKT-SKARTMYVDTLEKAYK 56
DB 43 DGEWMIMKORGRKAITDNDQSI-LDHNKLR---SQYTPASNNEYMTWDELERSAS 98
QY 57 SAERKCEE--PSSEENVDVSAATLNIPLEAG-----NSWSEI----- 94
DB 99 RAESCMEHGPAS-----LPSIGONLGAHMGRTPEFHVQSMYDEVDSFYREHC 152
QY 95 -----FELRGKYNNKGTSNIANMVDSDKLGAVVDCSG-----KTHVVCY 139
DB 153 NPYCFPCSGPV-----CTHYTVVATSNRIGCAINLCHNMNIWQIWKAVYLYCNY 206
QY 140 GPEAKGDGKTIYEGAPCSR-SDYGAG 166
DB 207 SPKGNMNGHAPYKHGRCSPSPSGG 234

RESULT 9

US-09-800-198-25
Sequence 25, Application US/09800198
Publication No. US20030087816A1
GENERAL INFORMATION:
APPLICANT: Vernet, Corine AM
APPLICANT: Fernandes, Elma
APPLICANT: Shinkels, Richard A
APPLICANT: Herimann, John L
APPLICANT: Majumder, Kumud
APPLICANT: Mishra, Vishna
APPLICANT: Mezes, Peter S
APPLICANT: Rastelli, Luca
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-697
CURRENT FILING DATE: 2001-03-05
CURRENT APPLICATION NUMBER: US/09/800,198
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/186,596
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 25
LENGTH: 300
TYPE: PRT
ORGANISM: Homo sapiens
US-09-800-198-25

Query Match 16.0% Score 160; DB 9; Length 300;
Best Local Similarity 25.5% Pred No 5.3e-08;
Matches 53; Conservative 31; Mismatches 66; Indels 58; Gaps 11;

QY 1 EGDYSLCOOREK---LDDMEKMEFELHNGYRAAFARNTKT-SKARTMYVDTLEKAYK 56
DB 43 DGEWMIMKORGRKAITDNDQSI-LDHNKLR---SQYTPASNNEYMTWDELERSAS 98
QY 57 SAERKCEE--PSSEENVDVSAATLNIPLEAG-----NSWSEI----- 94
DB 99 RAESCMEHGPAS-----LPSIGONLGAHMGRTPEFHVQSMYDEVDSFYREHC 152
QY 95 -----FELRGKYNNKGTSNIANMVDSDKLGAVVDCSG-----KTHVVCY 139
DB 153 NPYCFPCSGPV-----CTHYTVVATSNRIGCAINLCHNMNIWQIWKAVYLYCNY 206
QY 140 GPEAKGDGKTIYEGAPCSR-SDYGAG 166
DB 207 SPKGNMNGHAPYKHGRCSPSPSGG 234

RESULT 10

US-09-905-291A-285
Sequence 285, Application US/09905291A
Patent No US20020160374A1

GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Bernstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kjaevn, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2001-07-12
CURRENT APPLICATION NUMBER: US/09/905,291A
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
TYPE: PRT

ORGANISM: Homo Sapien
US-09-905-291a-285
Query Match 15.98; Score 159; DB 9; Length 463;
Best Local Similarity 28.68; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;
OY 13 LDDMKREFTELHNGYAAFAARYKTSKMTVYDCTLEEKAYSAKC---SEPSSE 68
DB 28 LIDDEKRLMVELHNLVLAQVSP--ASDILHRMDEELAAFAKAYAROCVMGHNKRGRR 85
OY 69 EENVDFSAATLNTLEAGNSWSEIFELRGVYNNKNGKTSNTANM-----VWDSHK 121
DB 86 GENLPAITDEGMDVPL-AMEEMHE-----REHNLISAATCSPGQMGCHYTQVWAKTER 139
OY 122 LGCAYVDCS-----GKTHV---VCQYGPBAGDKGTIYEGAPCSRCDYAGVYCDDDW 173
DB 140 ICGSGHFCEKLGQVEETINIELVLCNTEPPGVNKGKRPYOBSTPCSCP---SGYHC--- 192
OY 174 QNLIC 178
DB 193 KNSLC 197
RESULT 11
US-09-902-853-285
Sequence 285, Application US/09902853
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavitt, Ivar J.
APPLICANT: Mathew, Jennie P.
APPLICANT: Pao, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TIME OF INVENTION: Acids Encoding the Same
PRIORITY REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902, 853
PRIOR APPLICATION NUMBER: US/09/665, 350
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/143, 048
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/145, 698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146, 222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
US-09-902-853-285
Query Match 15.98; Score 159; DB 9; Length 463;
Best Local Similarity 28.68; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;
OY 13 LDDMKREFTELHNGYAAFAARYKTSKMTVYDCTLEEKAYSAKC---SEPSSE 68
DB 28 LIDDEKRLMVELHNLVLAQVSP--ASDILHRMDEELAAFAKAYAROCVMGHNKRGRR 85
OY 69 EENVDFSAATLNTLEAGNSWSEIFELRGVYNNKNGKTSNTANM-----VWDSHK 121
DB 86 GENLPAITDEGMDVPL-AMEEMHE-----REHNLISAATCSPGQMGCHYTQVWAKTER 139
OY 122 LGCAYVDCS-----GKTHV---VCQYGPBAGDKGTIYEGAPCSRCDYAGVYCDDDW 173
DB 140 ICGSGHFCEKLGQVEETINIELVLCNTEPPGVNKGKRPYOBSTPCSCP---SGYHC--- 192
OY 174 QNLIC 178
DB 193 KNSLC 197
RESULT 12
US-09-907-824-285
Sequence 285, Application US/09907824
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavitt, Ivar J.
APPLICANT: Mathew, Jennie P.
APPLICANT: Pao, James
APPLICANT: Paoni, Nicholas F.

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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,824
PRIOR APPLICATION NUMBER: 2001-07-17
PRIOR APPLICATION NUMBER: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
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PRIOR FILING DATE: 1999-12-02
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-824-285

Query Match      15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1,2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

QY 13 LDDDMREFTLHNGRAAFARNYKTSKMTYVYDCTLEKAYKSAKRC-----SEPPSSE 68
DB 28 LTDEKRLAYELNHLRYAQSPT--ASDMLHMRWDEELAAFAKAYARQCVMGHNKERGR 85
QY 69 EENDVFSATLTNIPLEAGNSWMSSEIFELRGKYNNKNGKTSINAM-----VMSHDK 121
DB 86 GENLFATIDGMDVPL-AMEEMHNE-----REHYNLSAATSCSPQMGCHTYVMAKTER 139
QY 122 LGCNAVDCS-----GSTYV-----VCQYGRPAKGGKTYEAPASGRSDGAGYCTDDDM 173
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QY 174 ONLNC 178
DB 193 KNSJC 197

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RESULT 13
US-09-907-841-285
Sequence 285, Application US/09907841
Publication No. US20020198366A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsens, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Klievin, Ivar J.
APPLICANT: Mathew, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,841
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
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PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-841-285

Query Match      15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1,2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

QY 13 LDDDMREFTLHNGRAAFARNYKTSKMTYVYDCTLEKAYKSAKRC-----SEPPSSE 68
DB 28 LTDEKRLAYELNHLRYAQSPT--ASDMLHMRWDEELAAFAKAYARQCVMGHNKERGR 85
QY 69 EENDVFSATLTNIPLEAGNSWMSSEIFELRGKYNNKNGKTSINAM-----VMSHDK 121

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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

Query Match      15.98; Score 159; DB 9; Length 463;
Best Local Similarity 28.68; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

OY      13 LDDDMREFTLHNGYRAAFARNYKTSKRTVYDCTLEEKAYSERK-----SEPSSE 68
DB      28 LTDEERRLVVELHNLHYRAOVSPT--ASDMLHRWDEELAAFAKAYAROCVWGHNRERR 85
OY      69 EENVDFSAATINIPLENGSNWSEIFELRGVYKNGKTSNIAM-----VYDSHK 121
DB      86 GENLFAITDEGADVPL-AMEEMHE-----REHYMLSATCSPGOMCGHYTOVWAKTER 139
OY      122 LGCAYVDCS-----GKTHV---VCQYGPAAKGDGTYIEBAPCSRCSYDAGVTCDDDM 173
DB      140 IGGSHFCKLQGVETIELVNCNIEPQNVKGRPYQEGTFCSCQP---SGYHC----- 192
OY      174 QNLIC 178
DB      193 KNSLC 197

RESULT 16
US-09-906-742-285
; Sequence 285; Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Bostein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eason, Dan L
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvarso, Ellen
; APPLICANT: Fogel, Sherman
; APPLICANT: Geor, Wei-Oiang
; APPLICANT: Geor, Hanspeter
; APPLICANT: Gerlicsen, Mary E.
; APPLICANT: Goddard, Paul J.
; APPLICANT: Grimsaid, Christopher J.
; APPLICANT: Gunney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavitt, Ivar J.
; APPLICANT: Mathier, Jenale P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumes, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
```

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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

Query Match      15.98; Score 159; DB 9; Length 463;
Best Local Similarity 28.68; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

OY      13 LDDDMREFTLHNGYRAAFARNYKTSKRTVYDCTLEEKAYSERK-----SEPSSE 68
DB      28 LTDEERRLVVELHNLHYRAOVSPT--ASDMLHRWDEELAAFAKAYAROCVWGHNRERR 85
OY      69 EENVDFSAATINIPLENGSNWSEIFELRGVYKNGKTSNIAM-----VYDSHK 121
DB      86 GENLFAITDEGADVPL-AMEEMHE-----REHYMLSATCSPGOMCGHYTOVWAKTER 139
OY      122 LGCAYVDCS-----GKTHV---VCQYGPAAKGDGTYIEBAPCSRCSYDAGVTCDDDM 173
DB      140 IGGSHFCKLQGVETIELVNCNIEPQNVKGRPYQEGTFCSCQP---SGYHC----- 192
OY      174 QNLIC 178
DB      193 KNSLC 197

RESULT 17
US-10-121-049-360
; Sequence 360; Application US/10121049
; Publication No. US20030022239A1
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```
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 360
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
US-10-121-049-360

Query Match      15.9%: Score 159; DB 9; Length 463;
Best Local Similarity 28.6%: Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

OY 13 LDDMRKEMFTELHNGYRAAFANRYTSKMTMYDCTLEKAYKSAEC-----SEPPSS 68
DB 28 LTDEKRLMVELHNLRYAQSPT--ASDMLHMRWDELAFAKAYARQCVGNKRGRR 85
OY 69 EENVDFSAATLNPLEAGNSWSEIFELRGKYNNKNGTSNIANN-----VMDSHDK 121
DB 86 GENLFATIDEGMDVPL-AMEEWNHE-----REHYNLSAATCSFGQMGCHYTQVWAKTER 139
OY 122 LGCAVVDGS-----GKTHV---VCQYGPFAKGDGKTIYEGAPCSRCSYDGAGVTCDDDM 173
DB 140 ICGSHFCEKLGVEETNIELVYCNTEPFGNVKGRPRYOGTGPCSOCP-----SGYHC----- 192
OY 174 QNLIC 178
DB 193 KNSLC 197

RESULT 18
US-10-123-904-360
Sequence 360, Application US/10123904
Publication No. US2003002238A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
```

```
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C54
CURRENT APPLICATION NUMBER: US/10/123,904
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 360
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
US-10-123-904-360

Query Match      15.9%: Score 159; DB 9; Length 463;
Best Local Similarity 28.6%: Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

OY 13 LDDMRKEMFTELHNGYRAAFANRYTSKMTMYDCTLEKAYKSAEC-----SEPPSS 68
DB 28 LTDEKRLMVELHNLRYAQSPT--ASDMLHMRWDELAFAKAYARQCVGNKRGRR 85
OY 69 EENVDFSAATLNPLEAGNSWSEIFELRGKYNNKNGTSNIANN-----VMDSHDK 121
DB 86 GENLFATIDEGMDVPL-AMEEWNHE-----REHYNLSAATCSFGQMGCHYTQVWAKTER 139
OY 122 LGCAVVDGS-----GKTHV---VCQYGPFAKGDGKTIYEGAPCSRCSYDGAGVTCDDDM 173
DB 140 ICGSHFCEKLGVEETNIELVYCNTEPFGNVKGRPRYOGTGPCSOCP-----SGYHC----- 192
OY 174 QNLIC 178
DB 193 KNSLC 197

RESULT 19
US-10-140-470-360
Sequence 360, Application US/10140470
Publication No. US20030022331A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C160
CURRENT APPLICATION NUMBER: US/10/140,470
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 360
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-470-360

Query Match      15.9%: Score 159; DB 9; Length 463;
Best Local Similarity 28.6%: Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;
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QY 13 LDDDMREFTLHNGYRAAFARNTKSKRTMYDCTLEEKAKSAKNC-----SEEPSSE 68
DB 28 LDEKRLMVELHNLHRAOVSPT--ASDMLHMRWDELLAFAFAIAVROCVMGHKKEGR 85
QY 69 BENVDYFSATLNTILEGNSWSEIFELRGKVTYNNKKTSTNAN-----VWDSHK 121
DB 86 GENLFAITDEGMVPL-AMEEMHHE-----REHYNLSAATCSFGQMGCHTYOVWAKTER 139
QY 122 LCCAVVDCS-----GKTHV---VCQYGEAKGDKTYEAGPCSRCSDDYAGVTCDDW 173
DB 140 ICGSHFCEKLGQVEETINELLYCNTEPPGNVKGKRPYOBETPCSOCP---SGYHC----- 192
QY 174 QNLIC 178
DB 193 KNSLC 197

RESULT 20
US-09-906-838-285
Sequence 285, Application US/09906838
Publication No. US20030027145A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottardo, A.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillen, Kenneth J.
APPLICANT: Kijavita, Ivar J.
APPLICANT: Mather, Jennie F.
APPLICANT: Pan, James
APPLICANT: Pooni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906, 838
PRIOR FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665, 350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143, 048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145, 698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146, 222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
US-09-906-838-285

Query Match 15 9% Score 159; DB 9; Length 463;
Best Local Similarity 28 6% Pct No 1 2e-07;
Matches 53; Conservative 72; Mismatches 72; Indels 34; Gaps 9;

QY 13 LDDDMREFTLHNGYRAAFARNTKSKRTMYDCTLEEKAKSAKNC-----SEEPSSE 68
DB 28 LDEKRLMVELHNLHRAOVSPT--ASDMLHMRWDELLAFAFAIAVROCVMGHKKEGR 85
QY 69 BENVDYFSATLNTILEGNSWSEIFELRGKVTYNNKKTSTNAN-----VWDSHK 121
DB 86 GENLFAITDEGMVPL-AMEEMHHE-----REHYNLSAATCSFGQMGCHTYOVWAKTER 139
QY 122 LCCAVVDCS-----GKTHV---VCQYGEAKGDKTYEAGPCSRCSDDYAGVTCDDW 173
DB 140 ICGSHFCEKLGQVEETINELLYCNTEPPGNVKGKRPYOBETPCSOCP---SGYHC----- 192
QY 174 QNLIC 178
DB 193 KNSLC 197

RESULT 21
US-09-907-613-285
Sequence 285, Application US/09907613
Publication No. US20030027145A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottardo, A.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillen, Kenneth J.
APPLICANT: Kijavita, Ivar J.
APPLICANT: Mather, Jennie F.
APPLICANT: Pan, James
APPLICANT: Pooni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey

```

; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US/09/907,613
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 285
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-613-285

Query Match      15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

QY 13 LDDMRKFTLHNGYRAAFANNTYTSKMTWYDCTLEKAYKSAEC-----SEEPSSE 68
DB 28 LTDEKRLMVELNLRAQVSP--ASDMLHMRDELLAFAKAYARQCWGHNRGR 85
QY 69 EBNVDFSAATLNIPLEAGNSWSEITELGKYNNKNGTNSIANM-----VMDSHDK 121
DB 86 GENFEATTDGMDVPL-ANEEWHNE-----REHYNLSAATCSPGQMGCHYTQYVMAKTER 139
QY 122 LGCAVVDG-----GKTHV---VCQYGPKEKDGKTIYEGAPSCRSRDYAGVTCDDDM 173
DB 140 IGCSSHCERLQGVETNIELLYCNYPEPQNVAGKRPYDEGIPCSQCP---SGYHC----- 192
QY 174 ONLLC 178
DB 193 KNSLC 197

RESULT 22
US-09-907-942-285
; Sequence 285, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
```

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; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kjaivin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 285
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-942-285

Query Match      15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
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Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;
QY 13 LDDMRBMTFELHNGYRAAFARNYTKSMRTWYDCTLEEKAYKSAEC-----SEPPSSE 68
DB 28 LTDEKRLMVELHNLRYAOSPT--ASDMLHMRDEDELAFAKAYAROCVWGHNKERRR 85
QY 69 EENVDFSAATLNIPLEAGNSWMSSEIFELRGKYVYKNGKTSNIANM-----VMDSHDK 121
DB 86 GENLFAITDEGMDVPL-AMEEWHNE-----REHYNLSAATCSFGOMCGHYTYVWAKTER 139
QY 122 LGCAYVDCS-----GKTHV---VCOYGPBAGDKGTIYEGAPCSRCSDYAGVTCDDDM 173
DB 140 ICGSHFCERKLGVEETNIELLVNCTEPGPNVKGKRPYOGFPCSOCP---SGYHC----- 192
QY 174 ONLJC 178
DB 193 KNSJC 197

RESULT 23
US-10-175-746-360
; Sequence 360, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Desnoyers, Luc
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 360
; LENGTH: 463
; TYPE: PRF
; ORGANISM: Homo Sapien
US-10-175-746-360

Query Match 15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

```

```

QY 13 LDDMRBMTFELHNGYRAAFARNYTKSMRTWYDCTLEEKAYKSAEC-----SEPPSSE 68
DB 28 LTDEKRLMVELHNLRYAOSPT--ASDMLHMRDEDELAFAKAYAROCVWGHNKERRR 85
QY 69 EENVDFSAATLNIPLEAGNSWMSSEIFELRGKYVYKNGKTSNIANM-----VMDSHDK 121
DB 86 GENLFAITDEGMDVPL-AMEEWHNE-----REHYNLSAATCSFGOMCGHYTYVWAKTER 139
QY 122 LGCAYVDCS-----GKTHV---VCOYGPBAGDKGTIYEGAPCSRCSDYAGVTCDDDM 173
DB 140 ICGSHFCERKLGVEETNIELLVNCTEPGPNVKGKRPYOGFPCSOCP---SGYHC----- 192
QY 174 ONLJC 178
DB 193 KNSJC 197

```

```

RESULT 24
US-10-176-918-360
; Sequence 360, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Desnoyers, Luc
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 360
; LENGTH: 463
; TYPE: PRF
; ORGANISM: Homo Sapien
US-10-176-918-360

Query Match 15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

```

```

QY 13 LDDMRBMTFELHNGYRAAFARNYTKSMRTWYDCTLEEKAYKSAEC-----SEPPSSE 68
DB 28 LTDEKRLMVELHNLRYAOSPT--ASDMLHMRDEDELAFAKAYAROCVWGHNKERRR 85
QY 69 EENVDFSAATLNIPLEAGNSWMSSEIFELRGKYVYKNGKTSNIANM-----VMDSHDK 121
DB 86 GENLFAITDEGMDVPL-AMEEWHNE-----REHYNLSAATCSFGOMCGHYTYVWAKTER 139
QY 122 LGCAYVDCS-----GKTHV---VCOYGPBAGDKGTIYEGAPCSRCSDYAGVTCDDDM 173
DB 140 ICGSHFCERKLGVEETNIELLVNCTEPGPNVKGKRPYOGFPCSOCP---SGYHC----- 192
QY 174 ONLJC 178
DB 193 KNSJC 197

```

```

RESULT 25
US-10-176-921-360
; Sequence 360, Application US/10176921
; Publication No. US20030027276A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Desnoyers, Luc
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.

```

```

APPLICANT:  Sherman, Steven
APPLICANT:  Smith, Victoria
APPLICANT:  Stewart, Timothy A.
APPLICANT:  Tumas, Daniel
APPLICANT:  Watanabe, Colin K
APPLICANT:  Wood, William
APPLICANT:  Zhang, Zemin
TITLE OF INVENTION:  SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE:  P330R1C288
CURRENT APPLICATION NUMBER:  US/10/176,921
PRIOR APPLICATION:  removed - See file Wrapper or Palm
SEQ ID NO 360
LENGTH:  463
ORGANISM:  Homo Sapien
US-10-176-921-360

Query Match      15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

QY 13 LDDDMREMTLHNGYRAFAARNYKTSKRTMYVDCITLSEKAYKSAEC-----SEEPSSE 68
DB 28 LTDEEKRLMVELHNLRYAQSPT--ASDMLHMRWDEELAFARQCVGHNKRGRR 85
QY 69 EENVDFSAATLNIPLDAGNSWSEIFELRGKYNNKNGKTSNIAM-----VWDSHDK 121
DB 86 GENLFAITDEGMDVPL-AMEEWNHE-----REHYNLSAATCSPGOMCGHYTOYVMKTER 139
QY 122 LGCAYVDCS-----GKTHV---VCOYGPBAGDGKTIYEGAPGRCSDYAGVTCDDDM 173
DB 140 ICGSHFCERKLGVEETINIELVYCNEPFGNVGKRPYOGFTCSQCP---SGYHC----- 192
QY 174 QNLIC 178
DB 193 KNSIC 197

RESULT 26
US-10-137-865-360
; Sequence 360, Application US/10137865
; Publication No. US20030032155A1
GENERAL INFORMATION:
APPLICANT:  Baker, Kevin P.
APPLICANT:  Beresini, Maureen
APPLICANT:  Desjardis, Laura
APPLICANT:  Desjardis, Luc
APPLICANT:  Filvaroff, Ellen
APPLICANT:  Gao, Wei-Qiang
APPLICANT:  Gerritsen, Mary E.
APPLICANT:  Goddard, Audrey
APPLICANT:  Godowski, Paul J.
APPLICANT:  Gurney, Austin L.
APPLICANT:  Sherwood, Steven
APPLICANT:  Smith, Victoria
APPLICANT:  Stewart, Timothy A.
APPLICANT:  Tumas, Daniel
APPLICANT:  Watanabe, Colin K
APPLICANT:  Wood, William
APPLICANT:  Zhang, Zemin
TITLE OF INVENTION:  SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE:  P330R1C154
CURRENT APPLICATION NUMBER:  US/10/137,865
PRIOR APPLICATION:  removed - See Palm or File Wrapper
SEQ ID NO 360
LENGTH:  463
TYPE:  PRT
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ORGANISM:  Homo Sapien
US-10-137-865-360

Query Match      15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

QY 13 LDDDMREMTLHNGYRAFAARNYKTSKRTMYVDCITLSEKAYKSAEC-----SEEPSSE 68
DB 28 LTDEEKRLMVELHNLRYAQSPT--ASDMLHMRWDEELAFARQCVGHNKRGRR 85
QY 69 EENVDFSAATLNIPLDAGNSWSEIFELRGKYNNKNGKTSNIAM-----VWDSHDK 121
DB 86 GENLFAITDEGMDVPL-AMEEWNHE-----REHYNLSAATCSPGOMCGHYTOYVMKTER 139
QY 122 LGCAYVDCS-----GKTHV---VCOYGPBAGDGKTIYEGAPGRCSDYAGVTCDDDM 173
DB 140 ICGSHFCERKLGVEETINIELVYCNEPFGNVGKRPYOGFTCSQCP---SGYHC----- 192
QY 174 QNLIC 178
DB 193 KNSIC 197

RESULT 27
US-10-140-474-360
; Sequence 360, Application US/10140474
; Publication No. US20030032156A1
GENERAL INFORMATION:
APPLICANT:  Baker, Kevin P.
APPLICANT:  Beresini, Maureen
APPLICANT:  Desjardis, Laura
APPLICANT:  Desjardis, Luc
APPLICANT:  Filvaroff, Ellen
APPLICANT:  Gao, Wei-Qiang
APPLICANT:  Gerritsen, Mary E.
APPLICANT:  Goddard, Audrey
APPLICANT:  Godowski, Paul J.
APPLICANT:  Gurney, Austin L.
APPLICANT:  Sherwood, Steven
APPLICANT:  Smith, Victoria
APPLICANT:  Stewart, Timothy A.
APPLICANT:  Tumas, Daniel
APPLICANT:  Watanabe, Colin K
APPLICANT:  Wood, William
APPLICANT:  Zhang, Zemin
TITLE OF INVENTION:  SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE:  P330R1C162
CURRENT APPLICATION NUMBER:  US/10/140,474
PRIOR APPLICATION:  removed - See Palm or File Wrapper
SEQ ID NO 360
LENGTH:  463
TYPE:  PRT
ORGANISM:  Homo Sapien
US-10-140-474-360

Query Match      15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

QY 13 LDDDMREMTLHNGYRAFAARNYKTSKRTMYVDCITLSEKAYKSAEC-----SEEPSSE 68
DB 28 LTDEEKRLMVELHNLRYAQSPT--ASDMLHMRWDEELAFARQCVGHNKRGRR 85
QY 69 EENVDFSAATLNIPLDAGNSWSEIFELRGKYNNKNGKTSNIAM-----VWDSHDK 121
DB 86 GENLFAITDEGMDVPL-AMEEWNHE-----REHYNLSAATCSPGOMCGHYTOYVMKTER 139
QY 122 LGCAYVDCS-----GKTHV---VCOYGPBAGDGKTIYEGAPGRCSDYAGVTCDDDM 173
DB 193 KNSIC 197
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; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 285
; TYPE: prt
; LENGTH: 463
; ORGANISM: Homo Sapien
US-09-904-859-285
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```

Query Match      15 98; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;
```

```

QY 13 LDDMRKREFTLHNGRAAFARNTKTSKMTVYDCTLEKAYSAKRC-----SEEPSSE 68
DB 28 LTDEKRLMVELHNLRAQVSP--ASDMLHMRWDEELAAFAKAYAROCVGHKNGRGR 85
QY 69 EENVDFSAATLNIPLEAGNSWMSSEIFELRGKYNNKNGTSNIANN-----VMDSHDK 121
DB 86 GENLFAITDEGMDVPL-AMEEMHNE-----REHYNLSAATCSPGOMCGHYTOVVMATKTER 139
QY 122 LGCAVNDCS-----GKTHV--VCQYGPFAKGDGKTIYEEGAPCSRSDYAGAVTCDDDW 173
DB 140 IGCSEHCCEKLOGVEETNIELVCNYPEPGRNVKGRKPYOEGTSCQCP---SGYHC----- 192
QY 174 ONLJC 178
DB 193 KNSJC 197
```

```

RESULT 30
US-09-909-204-285
; Sequence 285; Application US/09909204
; Publication No. US20030036061A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botschein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroft, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
```

```

; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US/09/909,204
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 285
; LENGTH: 463
; TYPE: prt
; ORGANISM: Homo Sapien
US-09-909-204-285
```

```

Query Match      15 98; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;
```

```

QY 13 LDDMRKREFTLHNGRAAFARNTKTSKMTVYDCTLEKAYSAKRC-----SEEPSSE 68
DB 28 LTDEKRLMVELHNLRAQVSP--ASDMLHMRWDEELAAFAKAYAROCVGHKNGRGR 85
QY 69 EENVDFSAATLNIPLEAGNSWMSSEIFELRGKYNNKNGTSNIANN-----VMDSHDK 121
DB 86 GENLFAITDEGMDVPL-AMEEMHNE-----REHYNLSAATCSPGOMCGHYTOVVMATKTER 139
```

```

      YQ    122 LGCAVNDGS-----GKTHV---VCQYGPBAGDKGTIERBAPCSRCDYGAVTCDDDW   173
          :|||              |||       |:||| |||:|
Db        140 IGGSGHCEKLGVEETNIELLVNCYNEBPNGVKRKRPYOBGFPCSQCP----SGYHC-----   192

      QY     174 ONLJC 178
          :|||
Db         193 KNSJLC 197


RESULT 31
US-10-142-431-360
Sequence 360, Application US/10142431
Publication No. US20030036179A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Flivauff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P33081C251
CURRENT FILING DATE: 2002-05-10
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 360
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-142-431-360

Query Match           15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

      QY     13 LDDDMREFTFELHNQYRAAFARNTSKMRTMYDCTLEEKAYSAKC-----SEEPSSE 68
          :|||              |||       |:||| |||:|
Db        28 LTDEKRIMWEHLNLHYRAOVSPT--ASDMLHRMWDELAAFAAKYAROCVGNHKRGRR 85

      QY     69 EEVDVPSAATLNPIPLEAGSNWSMEIFELRGKYNNKGKTSNIAM-----VMDSHDK 121
          :|||              |||       |:||| |||:|
Db        86 GENLFATIDEGMDVPL-AEMEWHNE-----REHYNLSAATSPOGMCHTYGVNAWKTER 139

      QY     122 LGCAVNDGS-----GKTHV---VCQYGPBAGDKGTIERBAPCSRCDYGAVTCDDDW   173
          :|||              |||       |:||| |||:|
Db        140 IGGSGHCEKLGVEETNIELLVNCYNEBPNGVKRKRPYOBGFPCSQCP----SGYHC-----   192

      QY     174 ONLJC 178
          :|||
Db         193 KNSJLC 197


RESULT 32
US-10-143-114-360
Sequence 360, Application US/10143114
Publication No. US20030036180A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen

```


APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijevlo, Ivar J.
APPLICANT: Kistner, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,700
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
US-09-906-700-285

Query Match 15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

13 LDDDMKEMTELHNGYRAAFARNYTSKRTMYDCTLEEKAKSAEC-----SEPPSS 68

DB 28 LTDEERKLAVELHNIYRAOVSPT--ASDMLHRMDEELAAFAAAYARQCVMGHNERRR 85
QY 69 EENVDFSAATLNIPLDGNMSWSEIFELRGVYKKNKNTSINLNM-----VWDSHK 121
DB 86 GENLFAITDEGADYPL-AMEBWHH-----REHYNLSAATCSPGQKCGHYTOYVAKTER 139
QY 122 LGCAYVDCS-----GKTHV---VCQYGPAPKAGDKTYIEBAPCSRCSDYAGAYTCDDDW 173
DB 140 ICGSHFCEKLGQVEETNIELVLCNTEPPGNVKGKRPYQEGTFCSCDP---SGYHC----- 192
QY 174 ONLTC 178
DB 193 KNSLC 197

RESULT 36
US-10-140-002-360
Sequence 360, Application US/10140002
Publication No. US20030037623A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 360
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-002-360

Query Match 15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

13 LDDDMKEMTELHNGYRAAFARNYTSKRTMYDCTLEEKAKSAEC-----SEPPSS 68
DB 28 LTDEERKLAVELHNIYRAOVSPT--ASDMLHRMDEELAAFAAAYARQCVMGHNERRR 85
QY 69 EENVDFSAATLNIPLDGNMSWSEIFELRGVYKKNKNTSINLNM-----VWDSHK 121
DB 86 GENLFAITDEGADYPL-AMEBWHH-----REHYNLSAATCSPGQKCGHYTOYVAKTER 139
QY 122 LGCAYVDCS-----GKTHV---VCQYGPAPKAGDKTYIEBAPCSRCSDYAGAYTCDDDW 173
DB 140 ICGSHFCEKLGQVEETNIELVLCNTEPPGNVKGKRPYQEGTFCSCDP---SGYHC----- 192
QY 174 ONLTC 178
DB 193 KNSLC 197

RESULT 37

```

US-09-902-903-285
Sequence 285, Application US/09092903
Publication No. US20030044839A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gierlsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Macher, Jenie P.
APPLICANT: Man, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,903
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien

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US-09-902-903-285
Query Match 15.9% Score 159; DB 9; Length 463;
Best Local Similarity 28.6% Pct. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9

OY 13 LDDMEEMETELHNGYAAAFANRYTISMTKMTMYDQTLLEKAYSAENC---SPESSSE 68
      | : : : | | | | | : : : | : : : | : : : | : : : | : : : |
Db 28 LTDEERLWELHMLHYIAQVSP--ASDMLHMKMDELLAAFAKAYIAQCWGNHNGRR 85
      | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
OY 69 EENVYVSATLNIPLFAGNSWMSIEFELGKTYKKNKGTSLNLM-----VYDSHDK 121
      | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 86 GENLFATDEGADVPL-AMEEWNHE-----REHYNLSAATSPSPQCMGHYTOYWATER 139
      | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
OY 122 LGCAYVYDCS-----GKTHV---VCQYGEAKGDKGTIYEGAPCSRSDYAGYTCDDW 173
      | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 140 ICGSHFECKKLGQVEETINELLVCHYEPENGVAKRPYQEGTSCPCP---SGYHC----- 192
      | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
OY 174 QNLIC 178
      | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 193 KNSLC 197
      | : : : | : : : | : : : | : : : | : : : | : : : | : : : |

RESULT 38
US-09-903-749A-285
Sequence 285, Application US/09903749A
Publication No. US20030045693A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fialyuroff, Ellen
APPLICANT: Fogel, Sherman
APPLICANT: Geo, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertelsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Mathier, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoul, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/903,749A
CURRENT FILING DATE: 2001-07-11
PRIORITY APPLICATION NUMBER: PCT/US00/04414
PRIORITY FILING DATE: 2000-02-22
PRIORITY APPLICATION NUMBER: US 60/143,048
PRIORITY FILING DATE: 1999-07-07
PRIORITY APPLICATION NUMBER: US 60/145,698
PRIORITY FILING DATE: 1999-07-26
PRIORITY APPLICATION NUMBER: US 60/146,222
PRIORITY FILING DATE: 1999-07-28
PRIORITY APPLICATION NUMBER: PCT/US99/20594
PRIORITY FILING DATE: 1999-09-08
PRIORITY APPLICATION NUMBER: PCT/US99/20944
PRIORITY FILING DATE: 1999-09-13
PRIORITY APPLICATION NUMBER: PCT/US99/21090
PRIORITY FILING DATE: 1999-09-15
PRIORITY APPLICATION NUMBER: PCT/US99/21547

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Page 21

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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/903,786
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR APPLICATION DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28314
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
US-09-903-786-285

Query Match      15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred No. 1,2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Caps 9.

13 LDDDKMEPTLEHGVAQAARNTSKMFTMYVDCITLKKRYKSAEFC-----SEEPSR 68
   ||||| ||||| |||||
28 LTDEKRILAVELHLYLRQVSPF--ASDMLMRWDELTAFAFAVAROCVGHNKERGR 85
   :|||:::|||||:
69 EENVVDFAAATLPIPLAGNSMWSEFFELDRKYNNKGKTSNIANNF-----YMSHDK 121
   ::|||:::|||||:
86 GENLFALTDEGMDVPL-AMEEMHE-----REHYNLNAAICSPFGMCIGHYTOVMWATER 139
   :|||:::|||||:
122 LGCAVVDCS-----GKNHV-----VCQGFPAEKDGKTIIEGGAFCSKSDYGAGVTCDDM 173
   :|||:::|||||:
140 ICGSHFECKLGVEENRIETLVCNTEPEPYNKGRKRYEGTSCSCP---SGVHC---- 192
   :|||:::|||||:

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RESULT 40
US-10-142-419-360
; Sequence 360, Application US/10142419
; Publication No. US20030044945A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Fillardoff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C244
; CURRENT APPLICATION NUMBER: US/10/142,419
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 360
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-419-360

Query Match          15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

DB 13 LDDNREMTFELHNGRAAFARNYTSKARTWYDCTLEKAYKSAEC-----SEPPSE 68
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 28 LTDEERKLWELHNYRAOVSP--ASDMLHMRWDELAFAKAYAROCVGNHKEGR 85
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 69 EENVDFSAATLNIPLDAGNSWMSSEIFELRGKYNNKNGKTSNIANK-----VMSHDK 121
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 86 GENLFAITDEGMVPL-AMEEWNHE-----REHYNLSAATCSPGOMCGHYTVVMAKTER 139
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 LGCWVWDCS-----GKTHV--VCQYGPPEAKGDKTIIEGAPCSRDYAGAVTCDDDW 173
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 140 ICGSHFCEKLGVEETNIELVCAVNEPFGNVKGRPFQESTPCSQCP---SGYHC----- 192
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 174 ONLGC 178
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 193 KNSLC 197
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 41
US-09-902-736-285
; Sequence 285, Application US/09902736
; Publication No. US20030049676A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fillardoff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, A.
```

```
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Peonli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,736
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 285
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-902-736-285

Query Match          15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

DB 13 LDDNREMTFELHNGRAAFARNYTSKARTWYDCTLEKAYKSAEC-----SEPPSE 68
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 28 LTDEERKLWELHNYRAOVSP--ASDMLHMRWDELAFAKAYAROCVGNHKEGR 85
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 69 EENVDFSAATLNIPLDAGNSWMSSEIFELRGKYNNKNGKTSNIANK-----VMSHDK 121
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 86 GENLFAITDEGMVPL-AMEEWNHE-----REHYNLSAATCSPGOMCGHYTVVMAKTER 139
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 122 LGCAYVDCS-----GKTHV---VCQYGPBANGDKRTIYEBGAFCSKSDYAGVTCDDM 173
Db 140 ICGSHFCEKLGVEETNIELVNCNTEPBNVKGKRPYQESTPCSCP-----SGYHC----- 192
QY 174 QNLIC 178
Db 193 KNSLC 197

RESULT 42
US-09-904-119-285
Sequence 285, Application US/09904119
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Iyar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,119
PRIOR FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/655,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
US-09-904-119-285

Query Match 15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1,2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

QY 13 LDDMRMFTLHNGRYRAFAFRNKTYSKMTWYDCTLEEKAYSAEKC-----SEEPSSE 68
Db 28 LTDEKRLWEHLNIXRQVSP--ASDMLHRMDELAARAKAYACVGMKNGRR 85
QY 69 EENVDFSAATINILEAGNSWSEIFELRGVYKRNKGTNINAM-----YVDSHK 121
Db 86 GENLFATIDEGMVFPL-AMEEMHE-----RETNLSAATCSPCOMCGHTVOYVAKTER 139
QY 122 LGCAYVDCS-----GKTHV---VCQYGPBANGDKRTIYEBGAFCSKSDYAGVTCDDM 173
Db 140 ICGSHFCEKLGVEETNIELVNCNTEPBNVKGKRPYQESTPCSCP-----SGYHC----- 192
QY 174 QNLIC 178
Db 193 KNSLC 197

RESULT 43
US-09-904-956-285
Sequence 285, Application US/09904956
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Iyar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,956
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048

```

; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 285
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-956-285

Query Match      15.9%  Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

QY 13 LDDMRMFTLHNGYAAFAFARNYKTSKRTMYDCTLEKAYSAKRC-----SEPPSS 68
DB 28 LTDERKRLMVELHNLRYAOVSPT--ASDMLHMRDEELAFKAYAROCVGNHKKRGR 85
QY 69 EENVDFSAATLNIPLEAGNSWSEIFELRGKYTNKNGKTSNIANN-----VMDSHDK 121
DB 86 GENLFAITDEGMDVPL-AHEEMHHE-----REHYNLSAATCSPQOMCGHYTQYVAKTER 139
QY 122 LGCAVNDCS-----GKTHV---VCQYSPKAGDKGKTYEEGAPCSRSDYGAGVTCDDW 173
DB 140 IGCSEHCEKLGVEERTINELVGNYPGNVNGKRPYOEGRPCSCP---SGYHC----- 192
QY 174 QNLIC 178
DB 193 KNSLIC 197

RESULT 44
US-09-907-794-285
; Sequence 285, Application US/09907794
; Publication No. US20030049677A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Geo, Wei-Qiang
```

```

; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, A. Paul J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kjaer, Jennie P.
; APPLICANT: Maier, Jennifer P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US/09/907,794
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 285
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-794-285

Query Match      15.9%  Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

QY 13 LDDMRMFTLHNGYAAFAFARNYKTSKRTMYDCTLEKAYSAKRC-----SEPPSS 68
DB 28 LTDERKRLMVELHNLRYAOVSPT--ASDMLHMRDEELAFKAYAROCVGNHKKRGR 85
QY 69 EENVDFSAATLNIPLEAGNSWSEIFELRGKYTNKNGKTSNIANN-----VMDSHDK 121
```

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Db      86 GENTRAITDEGMDVPL-AMEEWHHE-----REHYNLSTATCSPOQMGHYTQVWAKTER 139
OY      122 LGCAYVDCS-----GKTHV---VCQYGPBANKDGKTIYEGAPCSRSDYGAGVTCDDDW 173
Db      140 ICGSHFCEKIQVEETIELVLCNTEPPGNVKGKRPYOGTFCSCOP---SGYHC----- 192
OY      174 QNLIC 178
Db      193 KNSLC 197
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RESULT 45
US-10-123-262-360
: Sequence 360, Application US/10123262
: Publication No. US20030049816A1
```

```
GENERAL INFORMATION:
```

```
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerdtlen, Mary E.
APPLICANT: Goddard, Audrey J.
APPLICANT: Godowsky, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C38
: CURRENT APPLICATION NUMBER: US/10/123,262
: PRIOR FILING DATE: 2002-04-15
: PRIOR APPLICATION REMOVED - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 360
: LENGTH: 463
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-123-262-360
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```
Query Match      15.9% Score 159: DB 9: Length 463:
Best Local Similarity 28.6% Pred. No. 1.2e-07:
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;
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OY      13 LDDDMREMTFLHNGYRAAFARNYKTSKRPVYDCTLEKAYKSAEC-----SEPSSE 68
Db      28 LIDDEKRLMVLNHLNLYRAOVSPT--ASDYLHMRNDEELAFKAYARQCVMGHNKRGRR 85
OY      69 EENVDFSAATLNIPLAGSNWSEIFELRGVYNKNGKTSNIAM-----VYDSHDK 121
Db      86 GENTRAITDEGMDVPL-AMEEWHHE-----REHYNLSTATCSPOQMGHYTQVWAKTER 139
OY      122 LGCAYVDCS-----GKTHV---VCQYGPBANKDGKTIYEGAPCSRSDYGAGVTCDDDW 173
Db      140 ICGSHFCEKIQVEETIELVLCNTEPPGNVKGKRPYOGTFCSCOP---SGYHC----- 192
OY      174 QNLIC 178
Db      193 KNSLC 197
```

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Search completed: July 15, 2003, 08:37:15
Job time : 26 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2003, 08:32:08 ; Search time 40 Seconds
(Without alignments) 435,008 Million cell updates/sec

Title: US-09-937-555A-2

Sequence: 1 EGDYSLCQOERKLDLDDREM.....DYGAGVTCDDDMQNLCTGH 181

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR.73:*
2: PIR.1:*
3: PIR.2:*
4: PIR.3:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	290	29.1	274	2	A54419
2	209.5	21.0	246	2	T24493
3	190	19.1	425	2	C89753
4	154.5	15.5	207	2	T22436
5	153	15.3	213	2	T22439
6	152	15.2	212	2	T22437
7	146.5	14.7	208	2	T19852
8	143	14.3	207	2	T22438
9	142	14.2	210	2	T19849
10	140.5	14.1	211	2	T19859
11	139	13.9	262	2	T24854
12	138.5	13.9	209	2	T19848
13	137.5	13.8	209	2	T19847
14	137	13.7	243	2	B33329
15	133.5	13.4	207	2	T22432
16	132	13.2	245	2	S68691
17	127	12.7	243	2	A33329
18	124	12.4	196	2	T27833
19	122	12.2	266	2	JC5308
20	121.5	12.2	208	2	T20661
21	121	12.1	207	2	T31959
22	121	12.1	219	2	JC4131
23	121	12.1	243	2	JF0204
24	119.5	12.0	244	2	A92902
25	118	11.8	161	2	T23399
26	118	11.8	283	2	DB6143
27	113	11.3	163	2	T04969
28	112.5	11.3	227	2	A11085
29	112.5	11.3	385	2	T21763

30	112	11.2	204	2	B44583	venom allergen ant
31	111.5	11.2	202	2	B44583	venom allergen ant
32	110.5	11.1	206	2	B44583	venom allergen ant
33	110	11.0	213	2	B31085	antigen 5-3-precu
34	108.5	10.9	205	2	D44583	venom allergen ant
35	108.5	10.9	212	2	T27834	hypothetical prote
36	107	10.7	204	2	B37399	antigen 5-3-precu
37	107	10.7	212	2	T24999	hypothetical prote
38	106	10.6	204	2	B44583	venom allergen ant
39	105.5	10.5	208	2	G44583	venom allergen ant
40	105	10.5	202	2	T29676	hypothetical prote
41	105	10.5	241	2	T33397	hypothetical prote
42	105	10.5	312	2	T16435	hypothetical prote
43	103	10.3	204	2	C44583	venom allergen ant
44	103	10.3	212	2	T20581	hypothetical prote
45	101	10.1	212	2	B57350	venom allergen III

ALIGNMENTS

RESULT 1
A54419
neutrophil inhibitory factor precursor - Ancylostoma caninum
C:Species: Ancylostoma caninum
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
C:Accession: A54419
R:Moyle, M.; Foster, D.L.; McGrath, D.E.; Brown, S.M.; Laroche, Y.; De Meuter, J.;
J. Biol. Chem. 269, 10008-10015, 1994
A:Title: A hookworm glycoprotein that inhibits neutrophil function is a ligand of ti
A:Reference number: A54419; MUID:94193581; PMID:7908286
A:Accession: A54419
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-274 <MOY>
A:Cross-references: GB:I27427; NID:g440279; PIDN:AA27789.1; PID:g440280

Query Match 29.1%, Score 290; DB 2; Length 274;
Best Local Similarity 34.3%, Pred. No. 1.7e-18;

Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;

OY	14	DDDMREMTLHNGYRAAFARNY-----KTSKMTMYDCTL 50
DB	35	NDISIRLQFLAHMNGYRSKALGHSITSESDDDDDPGFLPFAFRASKMYLTDDEA 94
OY	51	EERAYKSAEKSE--PSEENVDVFAATLNI---PLEAGNSWSEIFEL-----R 98
DB	95	EKAYVMSARNCSDDSPPEGYDENKRIYFENSV-NISEALKAMISAKAFYLNKTRGE 153
OY	99	GKYYNKGKTSNINAWYDSHDKGAYVDC-----SGKT-----HYVQYQPE 142
DB	154	GVLYSNHDISNFANLAWDAKREKGVAVNCPGSEIDETNHDGTYATTIVVCHPKI 213
OY	143	AKGDKITIEGACRSCSDY 163
DB	214	NKTEGQPIKVGTPDCDSERY 234

RESULT 2

T24493
hypothetical protein T05A10.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C:Accession: T24493
R:Stulson, J.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z19898
A:Accession: T24493
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-246 <MIL>
A:Cross-references: EMBL:Z68108; PIDN:CAA92136.1; GSPDB:GNO0028; CESP:T05A10.5
A:Experimental source: clone T05A10

C:Genetics:
A:Gene: CESP:T05A10.5
A:Map position: X
A:Introns: 66/2; 142/3; 179/3; 208/2
C:Superfamily: cysteine-rich secretory protein 1

Query Match 21.0%; Score 209.5; DB 2; Length 246;
Best Local Similarity 27.2%; Pred. No. 2.4e-11;
Matches 59; Conservative 26; Mismatches 87; Indels 45; Gaps 7;

QY 6 LCQREKLDLDD-----MREMETLHNGYRAAFARVY-----KTSK 40
DB 29 LCQAPSMVYKDDGSGFQCNLSVSDVTRNFTLDEQHNFTYSRLAKGFENNGETNTSQPKASQ 88
QY 41 MRTWYDCTLEERKAYKSAK-----SEEPSSEENVDFSAAT---LNIPLEAGNSMW 91
DB 89 MIKERYDCMLERFAONMANNCVFANSAHYERPNOGNTLYMSSFSNPDRSLHTHVAEKW 148
QY 92 SEIFE-----LNGKYNNKNGKT-SNINAMVWDSHDKLCAVVDGSGKTHVCOYGE 142
DB 149 QELEERETPIDNVLPELMDLKRAIGHYQVAMDRYRLCGIANGPKMSYVCHYCPA 208
QY 143 AKGDKITYEEGAPCSRSDYAGVTCDDDMQMLCI 179
DB 209 GNKRNNKIYEIGDPCEVDDCPICIDCK--TTSICLV 243

RESULT 3
C89753
protein F11C7.3 (imported) - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
C:Accession: C89753
R:nonymus, The C. elegans Sequencing Consortium.
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; WUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_elegans
A:Accession: C89753
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1425 <SRO>
A:Cross-references: GB:chr_X; PIDN:MAC69015.1; PID:g29141420; GSPDB:GN00028; CESP:F11C7.3
C:Genetics:
A:Gene: F11C7.3
A:Map position: X

Query Match 19.1%; Score 190; DB 2; Length 425;
Best Local Similarity 23.0%; Pred. No. 2.6e-09;
Matches 45; Conservative 40; Mismatches 79; Indels 32; Gaps 5;

QY 4 YSLCQQRERKLDLDDREMETLHNGYRAAFARVYKTSK-----RTMYDCTL 50
DB 222 FTMCPSPVTDOSQARONFLDTHNKLRTSLAKGLADGIAAGAFAPMAKOMPKLYKSTCV 281
QY 51 EEAAYKSAEKSEEPSSEEE---NDVFSATLNIPL-----EAGNSMWSEIFE----- 96
DB 282 EANARWTWAKGCLYOHSTSAQRPGAGENTLYMINNPKIQTRAEDSSKAMWSEIKDFGVGS 341
QY 97 ---LRGKYNNKNGKTSNINAMVWDSHDKLCAVVDGSGKTHVCOYGEPEAKGDKITYEE 153
DB 342 DNILTOAVFDRG--VGHTQWAMEGTEICFEVENCPEFTYSVCOYPAQNYNNOLITRK 399
QY 154 GAPCSRSDYAGVTC 169
DB 400 GSPCTADADCPGTCTC 415

RESULT 4
T22436
hypothetical protein F49E11.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T22436
R:Baynes, C.
A:Submitted to the EMBL Data Library, March 1996
A:Reference number: T219564
A:Accession: T22436
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-207 <MII>
A:Cross-references: EMBL:T20308; PIDN:CAA94348.1; GSPDB:GN00022; CESP:F49E11.9
A:Experimental source: clone F49E11
C:Genetics:
A:Gene: CESP:F49E11.9
A:Map position: 4
A:Introns: 56/3; 102/3; 175/2
C:Superfamily: yellowjacket venom allergen 5

Query Match 15.5%; Score 154.5; DB 2; Length 207;
Best Local Similarity 26.6%; Pred. No. 1.6e-06;
Matches 49; Conservative 19; Mismatches 71; Indels 45; Gaps 7;

QY 23 ELHNGYRAAFARVYKTSK-----MRTWYDCTLEERKAYKSAKSEEPSSEEE--- 70
DB 26 DAHNLRSAIAKSTYVAKGTKEPATDKRKVYDSYVAASQNTYANTC---PTGHSKGTG 82
QY 71 -----NDVFSATLNIPLAGNSMWSEIFEIRGKYNNK-----NGKTSNANM 114
DB 83 YGENLYNWSYTSADVGSIDSYG---EIAAANKEKFEQDFGKSNAMDITLFGSIGHTATC 139
QY 115 VWDSDHDKLCAVVDGSG-----GKTHVCOYGEPEAKDGTITYEEBAPCSRSDYGAG 166
DB 140 ANAANSTSGCVKNCNGDASMMNMKNKIVCOYSPQNTMGRPIIKETTSKSSCS---GS 196
QY 167 VVCD 170
DB 197 TKCD 200

RESULT 5
T22439
hypothetical protein F49E11.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T22439
R:Baynes, C.
A:Submitted to the EMBL Data Library, March 1996
A:Reference number: T219564
A:Accession: T22439
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-213 <MII>
A:Cross-references: EMBL:T20308; PIDN:CAA94351.1; GSPDB:GN00022; CESP:F49E11.4
A:Experimental source: clone F49E11
C:Genetics:
A:Gene: CESP:F49E11.4
A:Map position: 4
A:Introns: 14/1; 60/3; 105/3; 175/2
C:Superfamily: yellowjacket venom allergen 5

Query Match 15.3%; Score 153; DB 2; Length 213;
Best Local Similarity 27.1%; Pred. No. 2.3e-06;
Matches 45; Conservative 29; Mismatches 64; Indels 28; Gaps 7;

QY 24 LNHNGYRAAF-----RNKYSKMTWYDCTLEERKAYKSAKSEEPS---SEEN 71
DB 31 VHNFRSOLALGOLFPGVKKPSASMMRKISMSKLLTNATKFAETCRKNSVVMNTGES 90
QY 72 VDVFSATLNIPL-----AGNSMWSEIFEIRG---KYNNKNGKTSNINAM---VWDSHDK 121
DB 91 IFMHRSSSLSPDEQVTLAPQKWMNE-FETNGMSLILYNASROIGHAVOMAMHTTSK 149
QY 122 IGCVAVDSCGKTH-----VWCOYGEPEAKGDKITYEEGAPCSRSD 162

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Db      150 VCGTSCAVGTPEQTMVYVYCNFKQNGIEGPIYNEGTCRKE 195

RESULT 6
T22437
hypothetical protein F49E11.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T22437
R:Baynes, C.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19564
A:Accession: T22437
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-212 <WIL>
A:Cross-references: EMBL:Z70308; PIDN:CAA94349.1; GSPDB:GN00022; CESP:F49E11.5
C:Experimental source: clone F49E11
C:Genetics:
A:Gene: CESP:F49E11.5
A:Map position: 4
A:Introns: 17/1; 146/3; 180/2
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match      15.2% Score 152; DB 2; Length 212;
Best Local Similarity 24.5%; Pred. No. 2.8e-06;
Matches 51; Conservative 25; Mismatches 92; Indels 40; Gaps 8;

Db      4 YSLGQREKLDMDRMETELNGYBAFA-----RNKTKSMRTMYDCTLEKA 54
      13 FSPCTCEPSTGRKYLIRSLNYLRQJALGVAGNSTRKSANMKLMDITLETTH 72
      55 YKSAEKSEPSSEENVD-----VPSAATLNIPLNGSNWSEIFELRGKYNNK 104
      73 ODYSTGCPHGSRAKNIGENMYMTSPVYTDALIELNRSANLMESE-FQRFQ-WNG 129
      105 NGKTSNIA-----MYWDSHDKLCAVVDSCGTH-----VYQYGPAPKAGDKRTI 151
      130 NLTEELPNSGIGHATQMAATNTNIGGICSSDSFQYQYVCLXSPAGNYIGMDIY 189
      152 EEGAPCSRCSDYAGVTCDDMQLICI 179
      190 KSGETCSNCPD---GTNCES-STGLCY 212

Db      130 VHNLTNRIRAKGYIAKGTAPASDMLKKMKWDATVPAASQAYANKCPTGSHGAAGLIGEN 89

RESULT 7
T19852
hypothetical protein C39E9.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T19852
R:Sims, M.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19187
A:Accession: T19852
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-208 <WIL>
A:Cross-references: EMBL:Z70307; PIDN:CAA94335.1; GSPDB:GN00022; CESP:C39E9.2
C:Experimental source: clone C39E9
C:Genetics:
A:Gene: CESP:C39E9.2
A:Map position: 4
A:Introns: 14/1; 59/3; 176/2
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match      14.7% Score 146.5; DB 2; Length 208;
Best Local Similarity 24.3%; Pred. No. 8.3e-06;
Matches 45; Conservative 26; Mismatches 63; Indels 51; Gaps 7;

Db      24 LHNQRAAPARNYKTSK-----MYWYDCTLEEKAYSAEKCEP----- 64
      30 VHNLTNRIRAKGYIAKGTAPASDMLKKMKWDATVPAASQAYANKCPTGSHGAAGLIGEN 89

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      65 -----PSSEENVDFSAATLNIPLNGSNWSEIFELRGKYNNKNGKTSNIA----- 113
      90 LMYWTSATITINDPFGA-----TGSAAKEKFFDYG--WSSNTLSMSLFTNGIGHA 139
      114 --MYWDSHDKLCAVVDSC-----GKTHVYCOYGPAPKAGDKRTIIEGAPCSRSDYGA 165
      140 TQMAAKRTNLICGVKNCGRDFTNGFNRKYVYCOYKPDQNYLNQNYTSGTSCSCP---S 196
      166 GVTCD 170
      197 GTSCE 201

Db      197 GTSCE 201

RESULT 8
T22438
hypothetical protein F49E11.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T22438
R:Baynes, C.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19564
A:Accession: T22438
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-207 <WIL>
A:Cross-references: EMBL:Z70308; PIDN:CAA94350.1; GSPDB:GN00022; CESP:F49E11.6
C:Experimental source: clone F49E11
C:Genetics:
A:Gene: CESP:F49E11.6
A:Map position: 4
A:Introns: 58/3; 104/3; 176/2
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match      14.3% Score 143; DB 2; Length 207;
Best Local Similarity 23.0%; Pred. No. 1.7e-05;
Matches 46; Conservative 24; Mismatches 62; Indels 60; Gaps 8;

Db      18 REMETELNGYBAFAARNYKTSK-----MYWYDCTLEEKAYSAEKCEPSE 68
      23 QQAIVDAHNKLSISANGTYVAKGTQKSGSNMRKIKWDATVATSONYANC---PTGH 79
      69 EE-----NVDVPSAATLNIPLNGSNWSEIFELRGKYNNKNGKTSN 110
      80 SGGSGYGENLYWYMTSGTIGNLDTFGPA-----ASSSWSE-----FOYGTGWSN 124
      111 -----IANWYDCTLEEKAYSAEKCEPSE-----GKTHVYCOYGPAPKAGDKRTI 150
      125 TLDMTFNTGIGHATQMAATNTNIGGICGVKNCGRDPSNGYKVAVYCOYKTPGNYLNQPI 184
      151 YEEGAPCSRCSDYAGVTCDD 170
      185 YQGGTCAACP---SGTVACD 201

Db      185 YQGGTCAACP---SGTVACD 201

RESULT 9
T19849
hypothetical protein C39E9.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T19849
R:Sims, M.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19187
A:Accession: T19849
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-210 <WIL>
A:Cross-references: EMBL:Z70307; PIDN:CAA94332.1; GSPDB:GN00022; CESP:C39E9.6
C:Experimental source: clone C39E9
C:Genetics:
A:Gene: CESP:C39E9.6

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A:Map position: 4
A:introns: 58/3; 178/2
C:Superfamily: yellowJacket venom allergen antigen 5

Query Match
Best Local Similarity 14.2%; Score 142; DB 2; Length 210;
Matches 48; Conservative 23; Mismatches 70; Indels 52; Gaps 8;

Oy 18 REMFELHNGVRAAFAR-NY-----KSKRTVYVCTCELEKAKYSAEKSEPSSE 68
Db 23 KSLIMAHNDIRSRIRAKGNTYAKGKRRESATNMLKKAKMSSLEDSQNTYANGCHQHSIN 82
Oy 69 EENV-----DYFS-----AATLNIPLDAGNSWSEIFELCKRYNN-----N 105
Db 83 DRTIEENLYWMSGDPSLDLRFKGKIVIA-----WDHEFQFQSMNSNFSLALN 133
Oy 106 GRTSNIANMWYDSDHDKLCAVYDSCG-----KTHVYCOYGPBAKGDKTIEEGAPC 157
Db 134 TGVAAHARQIAMAPLTGIGGVAKNCGDARRGGLFOVAIVCOYRVNGNEFFKNTYNSGATC 193
Oy 158 SRCSDDYAGAYTCD 170
Db 194 SACP---AGTSCE 203

RESULT 10
T19859
hypothetical protein F49E11.11 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T19859; T22441
R:Slms, M.
submitted to the EMBL data library, March 1996
A:Reference number: Z195187
A:Accession: T19859
A:Status: preliminary; translated from GB/EMBL/DBDUB
A:Molecule type: DNA
A:Residues: 1-211 <W12>
A:Cross-references: EMBL:Z70307; PIDN:CA94341.1; GSPDB:GN00022; CESP:F49E11.1111
A:Experimental source: clone C3969
R:Baynes C
submitted to the EMBL data library, March 1996
A:Reference number: Z19564
A:Accession: T22441
A:Status: preliminary; translated from GB/EMBL/DBDUB
A:Molecule type: DNA
A:Residues: 1-211 <W12>
A:Cross-references: EMBL:Z70308; PIDN:CA94354.1; GSPDB:GN00022; CESP:F49E11.1111
A:Experimental source: clone F49E11
C:Genetics:
A:Gene: CESP:F49E11.11
A:Map position: 4
A:introns: 15/1; 60/3; 179/2
C:Superfamily: yellowJacket venom allergen antigen 5

Query Match
Best Local Similarity 14.1%; Score 140.5; DB 2; Length 211;
Matches 47; Conservative 25; Mismatches 71; Indels 53; Gaps 8;

Oy 15 DDMRFELHNGVRAAFARNTKTSKMT-----WVYCTCEEKYAKSAEKSESP 65
Db 22 ESTQGFYIDLHNKLFRTSIKGYVAKGPTTAAGSNLLKKMKWOTLTATAGTFRNTCPRH 81
Oy 66 SESE---EN-----YDVSATATINPLEGNSWSEIFELRGVYKKNKNTSN 110
Db 82 SNAAGVGNLKYMKRSSLPSPSGNDIYG-----AASVAMQGEQOQG--WTFNFTQA 131
Oy 111 IAN-----HWWDSDHDLGCAVYDSC-----GKHVYCOYGPBAKGDKTIEEG 154
Db 132 LNTGICGHATQMAATYGLIGCGVAKNGCPDPELNNYRNVAVVCOYKAKGNTLGDITKSG 191
Oy 155 APCSRCSDYAGAYTCD 170

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Db      192 TTCACAP---TGTTCE 204

RESULT 11
T24854
hypothetical protein T12A7.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #ext_change 15-Oct-1999
C:Accession: T24854
R:lemard, N
submitted to the EMBL Data Library, June 1996
A:Reference number: T19943
A:Accession: T24854
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-262 <NLI>
A:Cross-references: EMBL:Z73911, PIDN:CA98140.1; GSPDB:GN00022; CESP:T12A7.3
A:Experimental source: clone T12A7
C:Genetics:
A:Gene: CESP:T12A7.3
A:Map position: 4
A:Introns: 86/2, 192/3, 231/2

Query Match      13.9%; Score 139; DB 2; Length 262;
Best Local Similarity 26.2%; Pred. No. 5.3e-05;
Matches 59; Conservative 20; Mismatches 66; Indels 80; Gaps 11.

OY      14 DDDREKETE---LHNGY-----RAAFARNYKT-----SKRRTMYDCTL 50.
Db      59 DEDDEHEFMENEVAFCNDGNCNNYVPPGSQLAG-NFYVTRRHTTKRAAGSNIKKFFVNATL 117
OY      51 EEKAYKSAEKCSEEPSEEBENVDFSAATLNIPLLEAGNSM-----S 92
Db      118 ERSAYSPFAOK--NPQSHS-----FIDIGENLFMHWSITRDQDENKYGPMALIS 163
OY      93 EIFELRKRYNKNKGTSTNI-----ANNVYDSHDKLGCAYVDCS-----GKTH 134
Db      164 WIKERFERKFPDSTNLTINDIFSGVGHATOMVADYOMCAASHEKRIHKRTGRPTIKIC 223
OY      135 VVCYGEPAKDGDKTIEYEGAFSCSDYAGAVTCDDDNQNLICI 179
Db      224 VCYHWPKRGNYLNEPIYLEGPGSKCE---SKKCDK-RTGLICI 262

RESULT 12
T19848
hypothetical protein C39E9.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #ext_change 18-Feb-2000
C:Accession: T19848
R:Sims, M.
submitted to the EMBL Data Library, March 1996
A:Reference number: T219187
A:Accession: T19848
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-209 <NLI>
A:Cross-references: EMBL:Z70307; PIDN:CA94331.1; GSPDB:GN00022; CESP:C39E9.5
A:Experimental source: clone C39E9
C:Genetics:
A:Gene: CESP:C39E9.5
A:Map position: 4
A:Introns: 58/3, 177/2
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match      13.9%; Score 138.5; DB 2; Length 209;
Best Local Similarity 24.7%; Pred. No. 4.5e-05;
Matches 46; Conservative 50; Mismatches 71; Indels 39; Gaps 7.

OY      18 REMETELHNGYRAAFARNYKT-----NRIVYDCTLEEKAYKSAEKCSEEPSE 68
Db      23 KQSMVNAHNAVNSISLAKGGEYVAKGTCKDASTNLKKRWKWNSTLQASQNVYNGCPMOSHSD 82

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OY 69 EENDVFSAAATLNIPL-----EAGNSMSEIFELRGKYNKNGKTSNIAN----- 113
DB 83 KSYGNLFMAVYSSPTTDDIKYVASAVDTWSE--FOFEG--WNKRFYTTALMNGIGHAT 139
OY 114 -MWDSDHDKLGCAGVVC-----SGKTHVCOYGPBKAQDKTIYEGAPCSRDYGC 164
DB 140 OAVASAGVOYGCAGKACGADSVRVSGYKATVCOYKVPNGYLFKNINYSAGKCSACP--- 196
OY 165 AGVTCG 170
DB 197 AGTSCG 202

RESULT 13
T19847
hypothetical protein C399.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T19847
R:Stim: M
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19187
A:Accession: T19847
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-209 <MTL>
A:Cross-references: EMBL:Z70307; PIDN:CAA94330.1; GSPDB:GN00022; CESP:C399.4
A:Experimental source: clone C399
A:Gene: CESP:C399.4
A:Map position: 4
A:Intons: 14/1: 60/3; 177/2
C:Superfamily: yellowjacket venom allergen 5

Query Match 13.8%; Score 137.5; DB 2; Length 209;
Best Local Similarity 24.3%; Pred. No. 5.5e-05;
Matches 46; Conservative 21; Mismatches 75; Indels 47; Gaps 7;

OY 18 REMFTLHNGYRAAFARNTK-----SKMTVYDCTLEKAYSAKCS----- 62
DB 25 QOFTVDLHNSFRKRLATGYTSINGTLKPAQSNIRKMSDSTLATSQTYANTCPTGFSMT 84
OY 63 -----EPPSESEENVDFSAATLNIPLDAGNSMSEIFELRGKYNKNGK----- 107
DB 85 QGTGENLYMRTTSANISGDIYGCA-----ASVSEQE--FOKYGATNYFSGELPDG 136
OY 108 TSNIANVWMDSHDKLGCAGVDCS-----GKTHVCOYGPBKAQDKTIYEGAPCSRDYGC 161
DB 137 VONGQMAWAKTMLVCGCGVKNCGKDSGLNKVAVCHYKPLGRYDQMITYAGTSCGCP 196
OY 162 DYAGAVTCG 170
DB 197 ---GTSCD 202

RESULT 14
B33329
cysteine-rich secretory protein 2 type I precursor - human
N:Alternate names: testis-specific protein
C:Species: Homo sapiens (man)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Jun-2000
C:Accession: B33329; S68682
R:Kasahara, N.; Gekke, J.; Brew, K.; Spurr, N.; Goodfellow, P.N.
Genetics 5, 527-534, 1989
A:Title: Cloning and mapping of a testis-specific gene with sequence similarity to a sp
A:Reference number: A33329; MUID:90129048; PMID:2613336
A:Accession: B33329
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-243 <KKS>
A:Cross-references: GB:M25532; NID:g339882; PIDN:AAA61220.1; PID:g339883
R:Kraetzschmar, J.; Haendler, B.; Eberspaecher, U.; Roosterman, D.; Donner, P.; Schleun
Eur. J. Biochem. 236, 827-836, 1996

A:Title: The human cysteine-rich secretory protein (CRISP) family. Primary structur
A:Reference number: S68682; MUID:96270732; PMID:8665901
A:Accession: S68682
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-243 <KRA>
A:Cross-references: EMBL:X95239; NID:g1262816; PIDN:CAA64526.1; PID:g1262817
C:Genetics:
A:Gene: GDB:TPX1
A:Cross-references: GDB:120760; OMIM:187430
A:Map position: 6p21-6qter
C:Superfamily: cysteine-rich secretory protein 1
F:1-20/Domains: signal sequence [status predicted <SR>]
F:21-243/Product: cysteine-rich secretory protein 2 type I [status predicted <MT>]

Query Match 13.7%; Score 137; DB 2; Length 243;
Best Local Similarity 26.5%; Pred. No. 7.3e-05;
Matches 49; Conservative 28; Mismatches 72; Indels 36; Gaps 9;

OY 18 REMFTLHNGYRAAFARNTKSMRTVYDCTLEKAYSAKCSSEPPSEEB----- 70
DB 38 RELVNR-HNELKAVSP--PASNMLKEMSVREVTNNAQRMANKCTIQHSDPEDRTSTRC 94
OY 71 NVDVFSAAATLNIPLDAGNSMSEIFELRGKYNKNGKTSN-----IANVWMDSHDKLCA 125
DB 95 GENLYMSDPTSSMSALQSWYDELDF---VYGVGKSPNVAVGHYTLQWLSYVQVCG 151
OY 126 VDC-----SGKTHVCOYGPBKAQDK--TIYEGAPCSRDYAGAVTCG-----D 172
DB 152 IAYCPNQDSLKXYVCOYCPAGNNNRKNTPYOQGTFCACCPD-----DCDGLCTNSCQ 206
OY 173 WQNL 177
DB 207 YODL 211

RESULT 15
T22432
hypothetical protein F49E11.10 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T22432
R:Baynes, C.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19564
A:Accession: T22432
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-207 <MTL>
A:Cross-references: EMBL:Z70308; PIDN:CAA94344.1; GSPDB:GN00022; CESP:F49E11.10
A:Experimental source: clone F49E11
A:Gene: CESP:F49E11.10
A:Map position: 4
A:Intons: 58/3; 104/3; 175/2
C:Superfamily: yellowjacket venom allergen 5

Query Match 13.4%; Score 133.5; DB 2; Length 207;
Best Local Similarity 26.1%; Pred. No. 0.00012;
Matches 46; Conservative 23; Mismatches 72; Indels 35; Gaps 7;

OY 25 HNGYRAAFARNTKSK-----MRTVYDCTLEKAYSAKCSSEPPSEEB---ENV 72
DB 30 HNTLRKIRKIGTYAKGTQKSPGTNLLKKMDSAVASAOYANGCPTGSHSDAGLGNL 89
OY 73 DVE-----SAATLNIPLDAGNSMSEIFELRGKYNKNGKTSNIAN-----VWMDSHD 120
DB 90 YWWTGSLGDLNLYGASASWKEFDYD--WKSNIAMTIDIFNGIGHATOMAKSN 147
OY 121 KLGCAGVDCS-----GKTHVCOYGPBKAQDKTIYEGAPCSRDYAGAVTCG 170
DB 148 LIQCGKDCGDSNGLNKVTVVCOYKPGQNFINGYIVYSGATSCGCP---SOTSCG 200

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RESULT 16

neutrophil granules matrix glycoprotein SGP28 precursor - human
C/Species: Homo sapiens (man)
C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
C/Accession: S68691; S74313; S68683
R/Fielden, L.; Cowland, J.B.; Johnsen, A.H.; Borregaard, N.
FEBS Lett. 380: 246-250, 1996
A/Title: SGP28, a novel matrix glycoprotein in specific granules of human neutrophils
A/Reference number: S68691; MID:96186934; PMID:8601434
A/Accession: S68691
A/Molecule type: mRNA
A/Residues: 1-245 <KJE>
A/Cross-references: EMBL:X94323; NID:g1213612; PIDN:CAA63984.1; PID:g1213613
A/Accession: S74313
A/Molecule type: protein
A/Residues: 33-83;96-143;165-217;221-226 <KJL>
R/Kretzschmar, U.; Haendler, B.; Eberspacher, U.; Roosterman, D.; Donner, P.; Schleut
Eur. J. Biochem. 236: 827-836, 1996
A/Title: The human cysteine-rich secretory protein (CRISP) family. Primary structure and
A/Reference number: S68681; MID:96270732; PMID:8665901
A/Accession: S68683
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-105;S',107-245 <KRA>
A/Cross-references: EMBL:X95240; NID:g1262818; PIDN:CAA64527.1; PID:g1262819
C/Genetics:
A:Gene: SGP28
C:Superfamily: cysteine-rich secretory protein 1
F:1-19/Domain: signal sequence #status predicted <NT>
F:20-245/Product: neutrophil granules matrix glycoprotein SGP28 #status predicted <NT>

Query Match 13.2%; Score 132; DB 2; Length 245;
Best Local Similarity 25.1%; Pred. No. 0.00021;

Matches 48; Conservative 22; Mismatches 77; Indels 44; Gaps 8;

QY 14 DDDMREMFETL-----HNGYRAA--ARNTSKRMRYDCTLEKAYK 56
DB 21 NEDNDPFTLTLTQTOVQREIVKHKELRAVSPARN-----MLKKNKKDAANAAR 75
QY 57 SAECSESESEENVDFSAATNIPLEAGNSMSEIFELRGVYN-----KNG 106
DB 76 WANCCNRHSNFRDRTSLKCGE-NLWMSAPSSMSQAIQSWFDYDFDGVGPKTPNA 134
QY 107 KTSNIAMWYDSDHKLGAAYVDCSG---KTHVVCQYGEAKGDKTI--YEGAPCSRC 160
DB 135 VGHYQVWYSSYLVGCGNAYCPNOKVLTXYVCQYCPAGNMANRUYVPEOGAPCASC 194
QY 161 SDYGAAGVTCDD 171
DB 195 PD-----NCCDD 200

RESULT 17

testis-specific protein - mouse
C/Species: Mus musculus (house mouse)
C/Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 29-Sep-1999
C/Accession: A33329
R/Raschke, M.; Gultknecht, J.; Brew, K.; Spurr, N.; Goodfellow, P.N.
Genomics 5: 527-534, 1989
A/Title: Cloning and mapping of a testis-specific gene with sequence similarity to a spe
A/Reference number: A33329; MID:90129048; PMID:2613236
A/Accession: A33329
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-243 <RAS>
A/Cross-references: GB:M25533; NID:g202126; PIDN:AAA0472.1; PID:g202127
C:Superfamily: cysteine-rich secretory protein 1

Query Match 12.7%; Score 127; DB 2; Length 243;
Best Local Similarity 24.9%; Pred. No. 0.00058;

Matches 49; Conservative 28; Mismatches 84; Indels 36; Gaps 9;

QY 11 EKLDMMREMF-----ELHNGYRAAPARNYTSKMTPTVYDCTLEKAYKSAEK 60
DB 21 EGDNDPFTSLTNOLOVQREIVKHKELRRSV--NPQSDILKMSISDATTNOKMANR 78
QY 61 CSEPSSESEENVDFSAATNIPLEAGNSMSEIFELRGVYN-----GRTSNA- 112
DB 79 CLEHSSKDDR-KINIRCGENLWSTDPILWSTVIO--SWYENEDFVYGVGAKPMSAV 134
QY 113 ---NMWYDSDHKLGAAYVDCSGKTHV---VCOYGEAPGDK--TIYEGAPCSRCSD 162
DB 135 GHYTLQWYSSFKICGCIACPNODLKYFYCHYCPGNVKKSTPYOQCTPCASCPN 194
QY 163 YGAGVTCDD--DMONL 177
DB 195 NCEGICITNCSDFEDL 211

RESULT 18

hypothetical protein ZK384.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C/Accession: T27833
R/Alincourt, R.
submitted to the EMBL Data Library, November 1996
A/Reference number: Z20427
A/Accession: T27833
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-116 <KJL>
A/Cross-references: EMBL:Z82092; PIDN:CA805010.1; GSPDB:GN00023; CESP:ZK384.1
A/Experimental source: clone ZK384
C/Genetics:
A:Gene: CESP:ZK384.1
A:Map position: 59/3; 157/2
A/Introns: 58/3; 95/3; 157/2
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 12.4%; Score 124; DB 2; Length 196;
Best Local Similarity 24.8%; Pred. No. 0.00082;

Matches 41; Conservative 25; Mismatches 77; Indels 22; Gaps 7;

QY 12 KLDDMREMFTELHNGYRAAFARNYTS-----KMTPTVYDCTLEKAYKSAECS 62
DB 17 QLSPNRQOVLDFHNKLRSQVALGVFSANGTIRPPARMERLYGOOFERLADYVADCP 76
QY 63 ---EPPSSESEENVDFSAATNIPLEAGNSMSEIFELRG--KYNNKNGKTSNIAMWY 116
DB 77 DGLEIPIGRNIGMNYTTRKV---IDALND--MAEFPVNCMLSTIYN--DTSISAASQWY 130
QY 117 DSHDKLGAAYVDCSG-KTHVVCQYGEAPGDKTIYEGAPCSRC 160
DB 131 AGKYVGGVARKCDPINVVVYCYOQNLVGRPIYREKGPCTAC 175

RESULT 19

testis-specific, vespid, and pathogenesis-related protein 1 precursor - human
C/Species: Homo sapiens (man)
C/Date: 01-May-1997 #sequence_revision 01-May-1997 #text_change 19-May-2000
C/Accession: J05308; PC4311
R/Rich, T.; Chen, P.; Furman, F.; Hynh, N.; Israel, M.A.
Gene 180: 125-130, 1996
A/Title: RVP-1, a novel human gene with sequence similarity to genes of diverse spe
A/Reference number: J05308; MID:97128816; PMID:8973356
A/Accession: J05308
A/Molecule type: mRNA
A/Residues: 1-266 <RVC1>
A/Cross-references: EMBL:X91911; NID:g1030052; PIDN:CAA63005.1; PID:g1030053
A/Accession: PC4311
A/Molecule type: protein


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Db      78 KLHPNTSGENITWGSPIRVS-----AIIWTEIDIDFTRICKKVCCHYOV 131
QY      115 VMSHRLCCAVYDC-----SGKTHVCOYGPBAGDKGT--IYEGAPCSRCSYD 164
Db      132 VMDSTKVCACVQFPPKVGSGDALNSGAFHICNYGP--GGNYPTWPKRGACSCAPN-- 187
QY      165 AGVTCDDDMQNLCT 179
Db      188 -----NDKCLDNLV 197

RESULT 23
JE0204
testicular protein tpx-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 21-Jul-2000
C:Accession: JE0204
A:Maeda, T.; Sakashita, M.; Ohba, Y.; Nakaniishi, Y.
Biochem. Biophys. Res. Commun. 248, 140-146, 1998
A:Title: Molecular cloning of the rat tpx-1 responsible for the interaction between spec
A:Reference number: JE0204; MUID:98340864; PMID:9675100
A:Accession: JE0204
A:Molecule type: mRNA
A:Residues: 1-243 <AAE>
A:Cross-references: DDBJ:AB009662; NID:93374579; PIDN:BA32029.1; PID:93374580
C:Comment: This protein functions as a cell adhesion protein for the association between
C:Genetics:
A:Map position: 17
A:Superfamily: cysteine-rich secretory protein 1

Query Match      12.1%; Score 121; DB 2; Length 243;
Best Local Similarity 25.2%; Pred. No. 0.002;
Matches 41; Conservative 24; Mismatches 66; Indels 32; Gaps 8;

QY      39 SKRRTVYCTLEKAYVSAKSC--SEPSSEENDVSAATLNIPLKAGN-----SWM 91
Db      57 SNLKEKNVYQAAAMAKMANCLHSESTEDKINICGLENLWSDIPSRMTYIQSWY 116
QY      92 SE-----IFLRKRYTNKGTSTNIAMWVDSHDKLGCAYVDCG---KTHVCOYGPBA 143
Db      117 EENENFVFGVAK--PSAVGHITQLVWTSFKEGCVATCPMODTLKIFYVCHICPMG 173
QY      144 KGDGK--TIYEGAPCSRCSYDYGAGVTCDD-----DMQNL 177
Db      174 NNVAKSTPYHGGTFCASCPN-----NCNDGLCTNSCDFDL 211

RESULT 24
A49202
cysteine-rich secretory protein-1 - mouse
N:Alternate names: CRISP-1
C:Species: Mus musculus (house mouse)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 29-Sep-1999
C:Accession: A49202
R:Haendler, B.; Kratzschmar, J.; Theuring, F.; Schlemming, W.D.
Endocrinology 133, 192-198, 1993
A:Title: Transcripts for cysteine-rich secretory protein-1 (CRISP-1; DE/AEG) and the nov
A:Reference number: A49202; MUID:93307144; PMID:8319566
A:Accession: A49202
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-244 <AAE>
A:Cross-references: GB:105559; NID:9309190; PIDN:AAA7460.1; PID:9309191
A:Experimental source: NMR, epididymis, salivary gland
A:Title: Sequence extracted from NCI backbone (NCBIN:134675, NCBI:134676)
C:Superfamily: cysteine-rich secretory protein 1

Query Match      12.0%; Score 119.5; DB 2; Length 244;
Best Local Similarity 25.4%; Pred. No. 0.0027;
Matches 51; Conservative 31; Mismatches 84; Indels 35; Gaps 10;

QY      3 DYSLCOORREKLD---DMRETFELHNGRAFAFANYTSMKRMVYDCTLEKAYKSAE 59

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Db      21 DSGOENRIEKLSTTKMSVOELIVSKHNOLRNWSPPS--GSDLKEMNYDAQVNAQMD 78
QY      60 KCEPSPSE-----ENDVFSATLNIPLKAGNSMSEIFELRGVYKN--NGKT 108
Db      79 KTFESHPIELRTTNRCGEN--LFMSYSLASMSAIOGMVYEDLYDVGPPQDPVY 136
QY      109 SNIANWVDSHDKLGCAYVDCG---KTHVCOYGPBAGDKGT--IYEGAPCSRCSYD 163
Db      137 GHYTOVWNSTFQVACVACPKRNPRLRYRYCHCPVGYOGLTTPYTADEPCASCPH 196
QY      164 GAGVTCDDDMQNLCT--IGH 181
Db      197 -----CEDG---LCTNSCGH 208

RESULT 25
T52399
pathogenesis-related protein homolog [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 03-Nov-2000
C:Accession: T52399
R:Kaneko, T.; Kato, T.; Sato, S.; Nakamura, Y.; Asamizu, E.; Tabata, S.
submitted to the EMBL Data Library, September 1999
A:Reference number: 226062
A:Accession: T52399
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-161 <KAND>
A:Cross-references: EMBL:AF000417; PIDN:BA802556.1
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 3
C:Superfamily: pathogenesis-related leaf protein

Query Match      11.8%; Score 118; DB 2; Length 161;
Best Local Similarity 26.1%; Pred. No. 0.0022;
Matches 41; Conservative 21; Mismatches 41; Indels 54; Gaps 8;

QY      13 LDDDEREFTELHNGR-----AFARNYTSKRTMYDCTL----- 50
Db      21 LAEDLQDFLEAHNEARNNEVGLDPLWMDVVAAYASVYANOR---INDCALVHNSGPG 76
QY      51 EERAYVSAKSCSEPS---SEENVDFSAATLNIPLKAGNSMSEIFELRGVYKNK 106
Db      77 ENIAVSGEMSAEDAAEMWINERKQYD-YDSNTCNDP-----NC 114
QY      107 KTS-NIANWVDSHDKLGCAYVDC--SGKTHVCOYGP 141
Db      115 GYCLHYTVYWKNTVRLGCAKAVVCSGCTFYTCYDP 151

RESULT 26
D86143
hypothetical protein F6p3.11 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: D86143
R:Thoenes, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alou
Chin, C.W.; Chung, B.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim
C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Meltz, R.; Marzli
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talt
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Ventner, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D86143
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-263 <STOC>
A:Cross-references: GB:AE005172; NID:99665145; PIDN:AAF97329.1; GSPDB:GN00141

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C:Genetics:
A:Map position: 1

Query Match 11.8%; Score 118; DB 2; Length 283;
Best Local Similarity 25.8%; Pred. No. 0.0044;
Matches 41; Conservative 22; Mismatches 60; Indels 36; Gaps 8;

QY 8 OOREKLDMDMEFTELHN-----GYRAAFRRNYSKMTWYDCTLEEK 53
DB 118 RRRNVRNARSRE-FLIHNIVRARVGEPPQMDRLAAVRFWMANGR---VSGRLVH- 171
QY 54 AKSAEKSEEPSESEENVDFSAATLN-ILEAGNSWSE--IPELRKYNNKNGTSN 110
DB 172 -----SNCPYGE-----NIFMAGKNMSPRLVNMADDEKFDYVGNCEPHHCGH 219
QY 111 IANWVWDSHDKLGCAVDCS-GKTHVCOYGEAKGDKGK 148
DB 220 YTOIVWDSHDKLGCAVDCSNGVYALCYVPENPTGE 256

RESULT 27

T04989

pathogenesis-related protein 1 precursor, 19.3k - Arabidopsis thaliana
N:Alternate names: protein T16L1.210

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 23-Apr-1998 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000

C:Accession: T04989; S71271
R:Bayan, R.; Obermaier, B.; Deutschenbaur, S.; Piravandi, E.; Hohenisel, J.; Mewes, H.W.;
submitted to the Protein Sequence Database, November 1998

A:Reference number: 215393
A:Accession: T04989

A:Molecule type: DNA
A:Residues: 1-163 <BEV>

A:Cross-references: EMBL:AL031394

A:Experimental source: cultivar Columbia; BAC clone T16L1

R:Kloska, S.; Schuster, W.
submitted to the EMBL Data Library, March 1996

A:Reference number: S71271
A:Accession: S71271

A:Molecule type: DNA

A:Residues: 1-77, 'P', '79-82', 'L', '84-88', 'RL', '91-92', 'RR', '95-162', 'LKENSF' <KLO>

A:Cross-references: EMBL:X96600; NID:g1228948; PID:g1228950

C:Genetics:

A:Gene: PRI

A:Map position: 4

A:Note: T16L1.210

C:Superfamily: pathogenesis-related leaf protein
F:1.26/Domain: signal sequence #status predicted <SIG>

F:27-163/Product: pathogenesis-related protein 1, 19.3k #status predicted <MAT>

Query Match 11.3%; Score 113; DB 2; Length 163;
Best Local Similarity 24.1%; Pred. No. 0.0064;
Matches 38; Conservative 23; Mismatches 53; Indels 44; Gaps 7;

QY 16 DMREMFTELHNGYR-----AAFAFYKTSKMTWYDCTLEEKAYKSEK 61
DB 28 DSPDFLAIVNRARAVYGVPLMDKAVKAAARVYANQKRG---DCAMKHS----- 76
QY 62 SEEPSSEENVDFSAATLN-ILEAGNSWSEIPELRKYNNKNGTSN 114
DB 77 -----GSGENIANSSSGSMGTG--AAVDMWVDEQFD-----YDSDNTCAMDKQGHATQ 125
QY 115 VWDSHDKLGCAVDCS-SGTHVCOYGEAKGDKGKTIY 151
DB 126 WVRNSERLGCAYKRCNNGQFTTCNDPDPGNWVGEWY 163

RESULT 28

A31085

antigen 5-2 precursor - bald-faced hornet

C:Species: Vespaula maculata (bald-faced hornet)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jan-2000
C:Accession: A31085

R:Fang, R.S.Y.; Vitale, M.; Fehlner, P.; King, T.P.
Proc. Natl. Acad. Sci. U.S.A. 85, 895-899, 1988

A:Title: cDNA cloning and primary structure of a white-face hornet venom allergen.

A:Reference number: A94213; MUID:88124947; PMID:3422469

A:Accession: A31085

A:Molecule type: mRNA

A:Residues: 1-227 <FAN>

A:Cross-references: GB:J03601; NID:g156714; PID:g156715

C:Superfamily: yellowjacket venom allergen antigen 5

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-227/Product: antigen 5-2 #status predicted <MAT>

Query Match 11.3%; Score 112.5; DB 2; Length 227;
Best Local Similarity 23.4%; Pred. No. 0.011; 74; Indels 27; Gaps 6;
Matches 39; Conservative 27; Mismatches 50

QY 13 LDDMEFTELHNGYRAAFRRNYSKMTWYDCTLEEKAYKSEK 61
DB 59 LTNDKNEILKRNHDFKONVAKGLETRKRGFPQPPAKNNVWNLAKIQTWANOCD 118
QY 62 -----SEEPSSEENVDFSAATLN-ILEAGNSWSEIPELRKYNNKNG---RTS 109
DB 119 FNHDDCRNTRAKYQVGNIAISITTAQDFPSKLIKQWEDVTEFNKYGLQNSFRVVG 178
QY 110 IANWVWDSHDKLGCA--VYDCSGKTH-VYCOYGEAKGDKGKTIY 152
DB 179 HYQWVWGTKEIKGSGIKYIEDNMYTHVLCVNGPGGNDPFIYE 225

RESULT 29

T21763

hypothetical protein F35E12.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T21763

R:Steward, C.
submitted to the EMBL Data Library, November 1996

A:Reference number: 219470

A:Accession: T21763

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-385 <HIL>

A:Cross-references: EMBL:281527; PID:CA04269.1; GSPDB:GN00023; CESP:F35E12.1

C:Genetics:

A:Gene: CESP.F35E12.1

A:Map position: 5

A:Intons: 103/1; 165/3; 210/3; 263/2; 342/2

Query Match 11.3%; Score 112.5; DB 2; Length 385;
Best Local Similarity 24.7%; Pred. No. 0.02;
Matches 36; Conservative 21; Mismatches 50; Indels 45; Gaps 7;

QY 23 ELHNGYRAAFRRNYSKMTWYDCTLEEKAYKSEK 64
DB 135 KIHNDLRSEIAGLEFLAKIEKPPASDMKISMDSIASEQFTIECPMNTKTEYGEN 194
QY 65 -----PSSEENVDFSAATLN-ILEAGNSWSEIPELRKYNNKNGTSN--- 113
DB 195 MHRWSKSEITDLDIYGT-----KRAESNAGE-FQKQWESNIYTKPTKESGIGHATQ 246
QY 114 MWDSHDKLGCAVDCS-----GKTHVCOY 139
DB 247 MWWSQAYLIGCGVCKGPDRTKRMKRIYVCY 280

RESULT 30

B44583

venom allergen antigen Ves g 5 - German yellowjacket

C:Species: Vespaula germanica (German yellowjacket)

C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 11-Jan-2000
C:Accession: B44583; A44522
R:Hoffman, D.R.


```
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in Hymenoptera venom XXV: the amino acid sequences of antigen 5 molec
A:Reference number: A44583; MOID:94044316; PMID:8227862
A:Accession: B44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>
C:Superfamily: yellowjacket venom allergen 5

Query Match      11.2%; Score 112; DB 2; Length 204;
Best Local Similarity 22.2%; Pred. No. 0.01;
Matches 39; Conservative 34; Mismatches 69; Indels 34; Gaps 7;

OY 4 YSLCOQREKIDDMREMFELHNGYRAAFARNT-----SKMTNVDCTLEERAKYSAEKS 53
DB 34 YGLTKROKQ--DLKE-----HNDFRKIRAGLETGRNGPQPPAKNNKMLVMSDELAVI 86
OY 54 AYKSAEKC-----SEEPSSEENVDFSAATLNIPLEAGNSWSEIFELR-GKYY 102
DB 87 AQVAMNQCOYGHDTCHDVAKYPGQNVALGSPAAKYDYPVLYVMWEDVKDYNPKKF 146
OY 103 NKNQ--RTSNIANMVMDSHDKLGA---VVDCSGKTHVCOYGPPEAKGDKGKTYEE 152
DB 147 SENNFLKIGHYQMWATKREVGCSIKYIQDKMKHNYLYCNGPAGNFGNEELYQ 202

RESULT 31
Venom allergen antigen Vesp c 5.02 - European hornet
C:Species: Vespula crabro (European hornet)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 11-Jan-2000
C:Accession: B44583; H44582
R:Hoffman, D.R.
A:Title: Allergens in Hymenoptera venom XXV: the amino acid sequences of antigen 5 molec
A:Reference number: A44583; MOID:94044316; PMID:8227862
A:Accession: B44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-202 <HOF>
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match      11.2%; Score 111.5; DB 2; Length 202;
Best Local Similarity 22.8%; Pred. No. 0.011;
Matches 37; Conservative 24; Mismatches 58; Indels 43; Gaps 5;

OY 25 HNGYRAAFARNT-----SKMTNVDCTLEERAKYSAEKC----- 61
DB 48 HNEFRQVARGLETGRNGPQPPAKNSMTLVNDELAIQAVMANOCYCHDCRSNAY 107
OY 62 -----SEEPSSEENVDFSAATLNIPLEAGNSWSEIFELR-GKYYNKNKTSNIAM 114
DB 108 SVGONIAEGSTADNFVNVMYK-----WEDVKDYQYGSPPKLNKLVGHYQ 158
OY 115 VMDSHDKLGA---VVDCSGKTHVCOYGPPEAKGDKGKTYEE 152
DB 159 VMATKREIGCSSEDTIEDGMHRYLYCNGPAGNFGNEPIYE 200

RESULT 32
Venom allergen antigen Ves vl 5 - yellowjacket (Vespula vidua)
C:Species: Vespula vidua
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 11-Jan-2000
C:Accession: B44583; E44522
R:Hoffman, D.R.
A:Title: Allergens in Hymenoptera venom XXV: the amino acid sequences of antigen 5 molec
A:Reference number: A44583; MOID:94044316; PMID:8227862
A:Accession: B44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-206 <HOF>

C:Superfamily: yellowjacket venom allergen antigen 5

Query Match      11.1%; Score 110.5; DB 2; Length 205;
Best Local Similarity 22.6%; Pred. No. 0.014;
Matches 38; Conservative 31; Mismatches 72; Indels 27; Gaps 7;

OY 13 LDDMREMFELHNGYRAAFARNT-----SKMTNVDCTLEERAKYSAEKS 62
DB 38 LYEAKROKILKVNHDEFQYAKGLETGRNGPQPPAKNNKMLVMSDELAVIAQVAMSCN 97
OY 63 --SEEPSSEENVDF-----FSATLNIPLEAGNSWSEIFELRGRY-YNKG--KTS 109
DB 98 YGHDTCKDTEKYPVGQNIARSTFALFDSPEKLYKKMEVDFNPINEMSKNNLKTG 157
OY 110 NIANNVMDSHDKLGA---VVDCSGKTH-VVCOYGPPEAKGDKGKTYEE 153
DB 158 HTQVWMAKREIGCSVKYKVDYTHLYCNGPAGNFRNEKLEYK 205

RESULT 33
Antigen 5-3 precursor - bald-faced hornet (fragment)
C:Species: Vespula maculata (bald-faced hornet)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jan-2000
C:Accession: B31085
R:Bang, K.S.Y.; Vitale, M.; Fehlner, P.; King, T.P.
A:Title: cDNA cloning and primary structure of a white-face hornet venom allergen, a
A:Reference number: A94213; MOID:88124947; PMID:3422469
A:Accession: B31085
A:Molecule type: mRNA
A:Residues: 1-213 <KAN>
C:Superfamily: yellowjacket venom allergen antigen 5
F:1-10/Domain: signal sequence #status predicted <SIG>
F:11-213/Product: antigen 5-3 #status predicted <MAT>

Query Match      11.0%; Score 110; DB 2; Length 213;
Best Local Similarity 23.4%; Pred. No. 0.016;
Matches 40; Conservative 30; Mismatches 67; Indels 34; Gaps 8;

OY 13 LDDMREMFELHNGYRAAFARNT-----SKMTNVDCTLEERAKYSAEKS 62
DB 46 VSNDEKNEIVNRHNOFQYAKGLETGRNGPQPPAKNNKMLVMSDELAKIAQVAMQCS 105
OY 63 -----SEEPSSEENVDFSA---ATLNIPLEAGNSWSEIFEL--RGVYNNK- 105
DB 106 FGHDCRNTERTERYQGVQNVAASTGNSYATWSKLTIE--KMEVDFNPCKTIGDNNF 162
OY 106 GRTSNIANMVMDSHDKLGA---VVDCSGKTH-VVCOYGPPEAKGDKGKTYEE 152
DB 163 SKVGHYQMWATKREIGCSVYIENMHYLYCNGPAGNFGNMDPIYE 213

RESULT 34
Venom allergen antigen Ves s 5 - southern yellowjacket
C:Species: Vespula squamosa (southern yellowjacket)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 11-Jan-2000
C:Accession: B44583; D44522
R:Hoffman, D.R.
A:Title: Allergens in Hymenoptera venom XXV: the amino acid sequences of antigen 5 m
A:Reference number: A44583; MOID:94044316; PMID:8227862
A:Accession: B44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-205 <HOF>
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match      10.9%; Score 108.5; DB 2; Length 205;
Best Local Similarity 23.3%; Pred. No. 0.021;
Matches 36; Conservative 29; Mismatches 67; Indels 29; Gaps 7;
```

QY 18 REAFTEHNGYRAAPFARNYKT-----SKARTMYDCTLEKAYKASEKC----- 61
 DB 42 KOELIKTHNDPFRNKVARGLETNGNGPOPPAKNNMNLVNNMELANIAQIVASOCKGHDPT 101
 QY 62 --SEPSSEENDVFSATNTIPLEAGN---SMWSEIFELRGKY---YNNKNGTSNAN 113
 DB 102 CKDTFTYNGVQNTAV--SSSTAAYVENGNLVKAMENEVDNPTLSWBNFETKIGHYTO 160
 QY 114 WYWDSDHKLGA---VVDSCGKTH-VVCQYGPAPKADGKTIVE 152
 DB 161 WMAKTRKICGSGIKYVDNNMYTHLVNVCYGFAGNGEYVE 203

RESULT 35

T27834
 hypothetical protein ZK384.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T27834
 R:Ainscough, R.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: 220427
 A:Accession: T27834
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-212 <MII>
 A:Cross-references: EMBL:Z82092; PIDN:CAB05011.1; GSPDB:GN00023; CESP:ZK384.2
 A:Experimental source: clone ZK384
 C:Genetics:
 A:Gene: CESP:ZK384.2
 A:Map position: 5
 A:Intons: 60/3; 106/3; 180/2
 C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 10.98; Score 108.5; DB 2; Length 212;
 Best Local Similarity 23.98; Pred. No. 0.022; 75; Indels 51; Gaps 9;
 Matches 47; Conservative 24; Mismatches 75; Indels 51; Gaps 9;

QY 9 OREILDNDMEFTELHNGYRAAPFARNY-----KTSKRTYVYDCTLEKAYKSAE 59
 DB 25 QREYD-----FHSLSQNLNGDIYVDGYPPRAKDKMKKWPILLAGAKKNNAA 75
 QY 60 KCSEPSSEEN-----VDVFSATNTIPLEAGNSWSEIFELRG---KY 102
 DB 76 TC--PSLFTDSKMLGRNTYHRLNAYVSGSLDKYALFAVKKWERO--FEERGMKNQEFRMF 131
 QY 103 NKNGTSNANWYWDSDHKLGAAYVDS-----GTHVVCQYGPAPKADGKTIVE 153
 DB 132 GDHRLTSATQWYMATRHVGGGVNICDAEKNLEGYRNNAVYICYSQKNGIHGLPYKE 191
 QY 154 GAPCSRCSIDYAGAVTCD 170
 DB 192 GPTCSACP---ASTKCE 205

RESULT 36

B37329
 antigen 5 - eastern yellowjacket
 C:Species: Vespula maculifrons (eastern yellowjacket)
 C>Date: 06-Nov-1992 #sequence_revision 06-Nov-1992 #text_change 11-Jan-2000
 C:Accession: B37329
 R:Li, G.; Villalba, M.; Coocla, M.R.; Hoffman, D.R.; King, T.P.
 submitted to the Protein Sequence Database, August 1992
 A:Reference number: A37329
 A:Accession: B37329
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-204 <STII>
 C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 10.78; Score 107; DB 2; Length 204;
 Best Local Similarity 21.68; Pred. No. 0.029; 70; Indels 34; Gaps 7;
 Matches 58; Conservative 34; Mismatches 70; Indels 34; Gaps 7;

QY 4 YSLCOQREKLDMDREKFEHNGYRAAPFARNYKT-----SKARTMYDCTLEK 53
 DB 34 YGLTKQEQ--DILKE-----HDFRQKTLARGLTRGNPGPPAKNNMNLVNSDELAVI 86
 QY 54 AYKSAEK-----SEPSSEENDVFSATNTIPLEAGNSWSEIFELRGKY 102
 DB 87 AQYMANOCQYGHDCRDVARYQGVNVALTGSTAAVYNDPVKLVKMEDEVDYNPKRKF 146
 QY 103 NKNG--KTSNANWYWDSDHKLGA---VVDSCGKTHVVCQYGPAPKADGKTIVE 152
 DB 147 SENNFLKIGHTYQWYVANTREVCGSGIKYIOENMHKHLVNCYGFAGNGEYVE 202

RESULT 37

T24999
 hypothetical protein T19C9.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
 C:Accession: T24999
 R:Matthews, L.
 submitted to the EMBL Data Library, March 1997
 A:Reference number: 219967
 A:Accession: T24999
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-212 <MII>
 A:Cross-references: EMBL:Z92972; PIDN:CAB07484.1; GSPDB:GN00023; CESP:T19C9.5
 A:Experimental source: clone T19C9
 C:Genetics:
 A:Gene: CESP:T19C9.5
 A:Map position: 5
 A:Intons: 64/3; 109/3; 176/2
 C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 10.78; Score 107; DB 2; Length 212;
 Best Local Similarity 18.78; Pred. No. 0.03; 58; Indels 58; Gaps 7;
 Matches 35; Conservative 36; Mismatches 58; Indels 58; Gaps 7;

QY 24 LNHGYRAAPFARNY-----KTSKRTYVYDCTLEKAYKSAEKSEPSSEENDVFS 76
 DB 37 IHNKLNAAASHGLMERHSISKSNQDLSMNSLVAENENKTYC--EPADNK----- 87
 QY 77 AATLNTIPLEAGNSWSEIFELRGKYNNKNGTSNANWYWDSDHKL----- 122
 DB 88 ---NLPIKLDN---IYQDVNTYDDIDGVGANGSINKDTHDLKSEAKAKNRLROM 139
 QY 123 -----GCAYVDSGKTH---VVCQYGPAPKADGKTIVEGAPCSRCSIDYGA 165
 DB 140 LYSKSKSICIVESCCKIDSKGINYTRLLICKYSPLENIDEKLDKGPSCNCP---S 196
 QY 166 GVTCD 172
 DB 197 GTCGTD 203

RESULT 38

A44583
 venom allergen antigen Ves f 5 - yellowjacket (Vespula flavopilosa)
 C:Species: Vespula flavopilosa
 C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 11-Jan-2000
 C:Accession: A44583; B44552
 R:Hoffman, D.R.
 J. Allergy Clin. Immunol. 92, 707-716, 1993
 A:Title: Allergens in hymenoptera venom XIV: the amino acid sequences of antigen 5
 A:Reference number: A44583; MUID:94044316; PMID:8227862
 A:Accession: A44583
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-204 <KQF>
 C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 10.68; Score 106; DB 2; Length 204;

A:Molecule type: DNA
A:Residues: 1-212 <KIR>
A:Cross-references: EMBL:U23514; NID:9746484; PID:9746485; PIDD:AA646538.1; CESP:F48B8.1
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:F48B8.1
A:introns: 28/1; 94/3; 153/3; 174/3; 226/3

Query Match 10.5%; Score 105; DB 2; Length 312;
Best Local Similarity 21.7%; Pred. No. 0.073; 80; Indels 38; Gaps 8;
Matches 41; Conservative 30; Mismatches 80

OY 1 EGDYSLCQOREKLDLDDREKTELENGYRAAFANNTYTSKRTMYVDCLEKAYKSAEK 60
DB 64 QDSGLSLRSHPREYIKKWTHEHRTKTR-----RMYASDMNKLWSDLAASQRRADT 119
OY 61 CSEEPSSEENV--DVSATLTIPLFAGNSMSEIFELR-GKYYNKNKTSNIANNVMD 117
DB 120 CDFRHSKRIVNGENIWAAPYSNYS-DALSTFNGHNPRGCGNHAYKHCCHYQVYVMA 178
OY 118 SHDKLGCAYDCS-----GKTH---VYCOYGEPAKGDGKTYT----- 151
DB 179 KTLVGCGRSDRYGVGWRGRHRYFVCHYMPQ-----GMTVYVTAAGOLYAMPFTWAS 234
OY 152 EECAPCSNC 160
DB 235 GDNGKCSNC 243

RESULT 43

C44583 allergen antigen Ves p 5 - western yellowjacket
Venom allergen antigen Ves p 5 - western yellowjacket
C:Species: 97-Jun-1994 penyalvanica (western yellowjacket)
C:Accession: C44583; C44522
R:Hoffman, D.R.
J:Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: C44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 10.3%; Score 103; DB 2; Length 204;
Best Local Similarity 20.6%; Pred. No. 0.066; 72; Indels 32; Gaps 5;
Matches 35; Conservative 31; Mismatches 72

OY 10 REKLDDMRKEMTELENGYRAAFANNTY-----SKRTMYVDCLEKAYKSAE 59
DB 38 KEKODILKE-----HNDFKIARLELRGNGPOPPAKNNKLVNDELAYVAQVWAN 92
OY 60 KC-----SEEPSSEENVDFSAATLTIPLFAGNSMSEIFELGK---VYNNK 106
DB 93 QCCYGHDCRDVAKYVGVQNVALTGSTADKIDNPKLYKMEDEVADYPRKFFSENNFN 152
OY 107 KTSNIANNVWDSHDKLGCAYDCS-----GKTHVYCOYGEPAKGDGKTYE 152
DB 153 KIGHYQVWANTKRIIGSGIKIYQNMENKHYLVGNTGSPGNFNGNELYO 202

RESULT 44

T20581
hypothetical protein F08E10.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T20581
R:gardner, A.
submitted to the EMBL Data Library, January 1998
A:Reference number: T20581
A:Accession: T20581
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-212 <ML>
A:Cross-references: EMBL:AL021566; PIDD:CAA16500.1; GSPDB:GN00023; CESP:F08E10.7
A:Experimental source: clone F08E10
C:Genetics:
A:Gene: CESP:F08E10.7
A:Map position: 5 109/3; 109/3; 176/2
A:introns: 64/3; 109/3; 176/2
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 10.3%; Score 103; DB 2; Length 212;
Best Local Similarity 19.3%; Pred. No. 0.069;
Matches 36; Conservative 35; Mismatches 58; Indels 58; Gaps 9;

OY 24 LKNGYRAAFANNTY-----KTSKRTMYVDCLEKAYKSAEKSEEPSSEENVDFVS 76
DB 37 IHNLRNMAASHGLMERYSISKSNMQLSWNESTLYAEVENEKRYC--EPADNK----- 87
OY 77 AATINIPLEAGNSMSEIFELRGKYYNK-----NGKTSN-----IANN 114
DB 88 -----NLTKLGDN-----IYQDVNTYDDIDGVAGMSIKRTHNHLASEKATRNLRQM 139
OY 115 VWDSHDKLGCAY-----VDCSGKTH---VYCOYGEPAKGDGKTYEAGAPCSRDYCA 165
DB 140 LYSKRSKISGICSDKIDSKININRFLYIKRYSPLNIDQLDNGEPCSNCP---S 196
OY 166 GVTCDDD 172
DB 197 GTSCGTD 203

RESULT 45

B37330
venom allergen III - red imported fire ant
N:Alternate names: allergen Sol I III
C:Species: Solenopsis invicta (red imported fire ant)
C:Date: 01-Oct-1992 #sequence_revision 01-Oct-1992 #text_change 11-Jan-2000
C:Accession: C44582; B60727; B37330
R:Hoffman, D.R.
J:Allergy Clin. Immunol. 91, 71-78, 1993
A:Title: Allergens in hymenoptera venom XXIV: the amino acid sequences of imported
A:Reference number: A44582; MUID:93139387; PMID:8423273
A:Accession: C44582
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-212 <HOF>
R:Hoffman, D.R.; Smith, A.M.; Schmidt, M.; Moffitt, J.E.; Guralnick, M.
J:Allergy Clin. Immunol. 85, 988-996, 1990
A:Title: Allergens in hymenoptera venom. Comparison of venoms from two species of
A:Reference number: B60727; MUID:90285439; PMID:2355158
A:Accession: B60727
A:Molecule type: protein
A:Residues: 1-3, 'X', '5', '8', 'X', '10', 'X', '12-15', 'X', '17-18', 'X', '20-23' <HOF>
C:Superfamily: yellowjacket venom allergen antigen 5
C:Keywords: venom

Query Match 10.1%; Score 101; DB 2; Length 212;
Best Local Similarity 24.6%; Pred. No. 0.1; 72; Indels 34; Gaps 6;
Matches 42; Conservative 23; Mismatches 72

OY 15 DDMREKTELENGYRAAFANNTY-----TSKRTMYVDCLEKAYKSAEKSEEP 64
DB 40 DAERKAIYKNHNELEDRVAGSKEMRGNGPOPPAYKPNLWDPDLATIAQMANOCTFE 99
OY 65 PSSEENVDFVS-----AAT-----LNIPLEAGNSMSEIFELRGKYYNKNKTSNI-- 111
DB 100 HDA-CRNERFAVQONIAATSSGKRNKSTPNEMILLVNEVKNDFNNKATSSFPDDDIIL 158
OY 112 -----ANNVWDSHDKLGCAYV-----DCSGKTHVYCOYGEPAKGDGKTYE 152
DB 159 KVEHYQVWANTKRIIGSGIKIYQNMENKHYLVGNTGSPGNFNGNELYO 209

Tue Jul 15 09:48:48 2003

us-09-937-555a-2.rpr

Page 14

Search completed: July 15, 2003, 08:34:55
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: July 15, 2003, 08:32:07 ; Search time 23 seconds
(without alignments)

326,401 Million cell updates/sec

Title: US-09-937-555a-2

Sequence: 1 EGDYSLCQGRKEDDDMMREM.....DYGAVTDDDDMMNLCLIGH 181

Scoring table: BIOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26.5	26.6	424	1	ASP_ANCCA
2	14.5	14.4	245	1	CRS3_HORSE
3	13.7	13.8	242	1	HELO_HELMO
4	13.7	13.7	243	1	TPX1_HUMAN
5	13.5	13.5	245	1	CRS3_HUMAN
6	12.7	12.7	243	1	TPX1_MOUSE
7	12.2	12.2	206	1	VA5_FOLDO
8	12.2	12.2	266	1	GLIF_HUMAN
9	11.5	12.0	244	1	AEGL_MOUSE
10	11.5	11.3	227	1	VA52_DOLMA
11	11.2	11.2	204	1	VA5_VESCR
12	11.1	11.1	202	1	TPX1_CAVPO
13	11.1	11.1	206	1	VA5_VESYI
14	11.0	11.1	205	1	VA5_VESSE
15	10.8	10.8	215	1	VA53_DOLMA
16	10.8	10.8	215	1	CRVP_TIRMU
17	10.7	10.7	183	1	VA5_VESMC
18	10.6	10.6	204	1	VA5_VESCR
19	10.6	10.6	202	1	VA51_VESCR
20	10.5	10.5	312	1	VR81_CAREL
21	10.5	10.3	312	1	VA5_VESBE
22	10.3	10.3	227	1	VA5_VESYU
23	10.3	10.1	241	1	ABE2_MOUSE
24	10.1	10.1	203	1	VA5_VESLA
25	10.0	10.1	203	1	VA5_VESLA
26	9.6	9.6	175	1	PRIA_LITES
27	9.6	9.6	234	1	VA3_SOLIN
28	9.5	9.5	211	1	VA3_SOLIN
29	9.5	9.5	205	1	VA5_POLPU
30	9.5	9.5	299	1	COH9_YEAST
31	9.5	9.5	167	1	PRI_SANNI
32	9.4	9.4	249	1	CRS1_HUMAN
33	9.4	9.4	204	1	SC7_SCHCO

34	9.4	9.4	246	1	AEG_RAT	P12020 rattus norv
35	9.3	9.3	164	1	PRI3_HORVU	P35792 hordeum vul
36	9.3	9.3	164	1	PRI3_HORVU	P35793 hordeum vul
37	9.2	9.2	202	1	VA5_VESMA	P81657 vespa manda
38	9.2	9.2	168	1	PRI3_TORAC	P08299 nicotiana t
39	8.9	8.9	164	1	PRI3_HORVU	P05968 hordeum vul
40	8.6	8.6	205	1	VA5_POLEX	P35759 polistes ex
41	8.6	8.6	209	1	VA5_POLEX	P05109 polistes ex
42	8.6	8.6	799	1	ITB5_HUMAN	P18084 homo sapien
43	8.5	8.5	161	1	PRI3_ARATH	P33154 arabidopsis
44	8.5	8.5	168	1	PRI3_TORAC	P09042 nicotiana t
45	8.3	8.3	168	1	PRI3_TORAC	P07053 nicotiana t

ALIGNMENTS

RESULT 1	ASP_ANCCA	STANDARD	PRT	424 AA.
ID	ASP_ANCCA			
AC	016937			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Ancyllostoma secreted protein precursor.			
GN	ASP.			
OS	Ancyllostoma caninum (Dog hookworm).			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;			
OC	Ancyllostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.			
OX	NCBI_Taxid:91170;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:96215086; PubMed:8636085;			
RA	Hardon J.M., Jones B.F., Hoffman D.R., Hotez P.J.;			
RT	"Cloning and characterization of Ancylostoma-secreted protein. A			
RT	novel protein associated with the transition to parasitism by			
RT	infective hookworm larvae."			
RT	J. Biol. Chem. 271:6672-6678(1996).			
RL	-1- FUNCTION: ASSOCIATED WITH THE TRANSITION TO PARASITISM BY			
CC	INFECTIVE HOOKWORM LARVAE.			
CC	-1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;			
CC	INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.			
CC	-----			
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CC	-----			
CC	EMBL: U26187; AAC47001.1; ..			
CC	HSP: P04284; ACCE.			
DR	Interpro: IPR001283; Allrgn_V5/TPX1.			
DR	Interpro: IPR001867; SCP; 1.			
DR	PRINTS: PRO0837; VSTPLIKE.			
DR	PRODOM: PD000542; Allrgn_V5/TPX1; 2.			
DR	SMART: SM00198; SCP; 2; AG5_PRI_SCP_1; FALSE_NEG.			
DR	PROSITE: PS01009; SCP_AG5_PRI_SCP_1; FALSE_NEG.			
DR	PROSITE: PS01010; SCP_AG5_PRI_SCP_2; FALSE_NEG.			
KW	SIGNAL.			
FT	FT			
FT	CHAIN 1 18			
FT	SEQUENCE 424 AA; 45735 MW; 4BC8295F5D3035F9 CRC64;			
FT	POTENTIAL.			
FT	ANCYLOSTOMA SECRETED PROTEIN.			
Query Match	26.6%; Score 265.5; DB 1; Length 424;			
Best local similarity	32.5%; Pred. 10.2e-16;			
Matches	62; Conservative 27; Mismatches 71; Indels 31; Gaps 6;			
QY	7 COOREKLDDREKRETELNGYRAAFARNT-----KTSKRTVWDCLEEKAVK 56			
DB	227 CPSNMTDSVDFTSVNFRSSVARGLEPPALGONAPKAAKMKVYKCEVESAIR 286			

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QY 57 SAEXSEPSSEEE---NDVFSAAITNI-----PLEAGNSWSEIFE-----LNG 99
DB 287 HGNKCYAOSHGHEDRPGENITYTSYLAKEFNKAKAQAOLAMNNEKEGCVPSNVLT 346
QY 100 KYVKNKG-KTSNIAMVWDSDKLGCAVVDSCGKTHVVCQYGPAPKADGKTIYEGAGCS 158
DB 347 ALNMRFGMOIGHYTMADDTYKLGCAVVCNDFTFGVCQYGPAGNMGHVITYMGPCS 406
QY 159 RCDSDYAGAVTC 169
DB 407 QCS---PGATC 414

RESULT 2
CRS3_HORSE
ID CRS3_HORSE STANDARD: PRT: 245 AA.
AC 019010:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cysteine-rich secretory protein-3 precursor (CRISP-3).
GN CRISP3
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ampulla;
RX MEDLINE=98422318; PubMed=9748582;
RA Schumbody A., Gentzel M., Wolles H., Ralda M., Neumann U.,
RA Toefter-Petersen E.;
RT "Equine CRISP-3: primary structure and expression in the male genital
RL tract.";
RT Blochim. Biophys. Acta 1387:206-216(1998).
CC -1- SUBCELLULAR LOCATION: SECRETED; IN NETTROPHILS. LOCALIZED IN
CC SPECIFIC GRANULES (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE SALIVARY GLAND, IN THE
CC AMPULLA AND THE SEMINAL VESICLE.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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CC -----
DB EMBL: AJ001400; CA004729.1; -
DR HSSP; P04284; ICFE.
DR InterPro: IPR001283; Allrgn_V5/TPX1.
DR Pfam: PF00188; SCP_1.
DR PRINTS; PR00837; VTPXLIKE.
DR PRODOM; PD000542; Allrgn_V5/TPX1. 1.
DR SMART; SM00198; SCP_1.
DR PROSITE; PS01009; SCP_AGS_PRL_SCP_1; 1.
DR PROSITE; PS01010; SCP_AGS_PRL_SCP_2; 1.
KW SIGNAL; Multigene family.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 245 CYSTEINE-RICH SECRETORY PROTEIN-3.
SQ SEQUENCE 245 AA; 27308 MW; 893AAEB7F402BA22 CRC64;

Query Match 14.4%; Score 143.5; DB 1; Length 245;
Best Local Similarity 26.4%; Pred. No. 8e-06; 76; Indels 33; Gaps 8;
Matches 48; Conservative 25; Mismatches 33; Indels 33; Gaps 8;

QY 16 DKREMTFLANGYRAAFARNTKTSKRTVYDCTLEEKAYKSAKSEPSSEENV--- 72
DB 36 EVCKEYVNHNDLRTVSP--LASNMKQWDSKTRATNAQWMAKCLLOHSAKEDRAVGT 93
QY 73 ----DVFSAAITNIPLEAGNSWSEIFEELRGKYVKNKGKTSN-----IANVWDSHDKL 122
```

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DB 94 MKCGENFMSSTIPMSSDAIQWMDHEVDFK---YGVGRTPNAVGHYTYVWYSSYRV 150
QY 123 GCAVVDSCGKTHVVCQYGPAPKADGK--TIYEGAPCSCSDYAGVTCDDDMQNL 176
DB 151 GCGIAYCPKQGTILKYYVVCQYCPAGNMYNKNINFPYEGCTPCARCPC-----NCD---NG 201
QY 177 LC 178
DB 202 LC 203

RESULT 3
HELIO_HELIO
ID HELIO_HELIO STANDARD: PRT: 242 AA.
AC 091055;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Heliothermine precursor (HITX)
OS Heloderma horridum horridum (Mexican beaded lizard).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosaurs; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;
OC Heloderma.
OX NCBI_TaxID=8552;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC TISSUE=Salivary gland;
RX MEDLINE=95375162; PubMed=7647234;
RA Morrisette J., Kraetzschmar J., Haendler B., El-Hayek R.,
RA Mochca-Morales J., Martin B.M., Patel J.R., Moss R.L.,
RA Schlenker W.-D., Coronado R., Possani L.D.;
RT "Primary structure and properties of heliothermine, a peptide toxin
RT that blocks ryanodine receptors.";
RT Biophys. J. 68:2280-2288(1995).
RN [2]
RP SEQUENCE OF 20-39, AND CHARACTERIZATION.
RC TISSUE=Venom;
RX MEDLINE=90260878; PubMed=1693019;
RA Mochca-Morales J., Martin B.M., Possani L.D.;
RT "Isolation and characterization of heliothermine, a novel toxin from
RT Heloderma horridum horridum (Mexican beaded lizard) venom.";
RT Toxicon 28:299-309(1990).
CC -1- FUNCTION: Toxin that blocks ryanodine receptors. It is toxic to
CC mice; it causes lethargy, partial paralysis of rear limbs and
CC lowering of body temperature.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Produced by the venomous gland.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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CC -----
DB EMBL: U13619; AAC59730.1; -
DR InterPro: IPR001283; Allrgn_V5/TPX1.
DR Pfam: PF00188; SCP_1.
DR PRINTS; PR00837; VTPXLIKE.
DR PRODOM; PD000542; Allrgn_V5/TPX1. 1.
DR SMART; SM00198; SCP_1.
DR PROSITE; PS01009; SCP_AGS_PRL_SCP_1; 1.
DR PROSITE; PS01010; SCP_AGS_PRL_SCP_2; FALSE_NEG.
KW Calcium channel inhibitor; Neurotoxin; Toxin; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 242 HELIOTHERMINE.
SQ SEQUENCE 242 AA; 27493 MW; 0E183FC2925DF3C CRC64;

Query Match 13.8%; Score 137.5; DB 1; Length 242;
```

Best Local Similarity 27.6%; Pred. No. 2.7e-05;
Matches 51; Conservative 23; Mismatches 72; Indels 39; Gaps 11;

OY 16 DNRETEHLNGYBAFARARYKTSKRTVYDCTLEKAYSAKES-DEPSEEEVND-73
DB 34 DQETETKRNHNLRRIEPT--ASNLMKWTMSNNIAONANOSANOCTLEHTSKERTIDG 91
OY 74 -----VFSA--TLNIPLEAGNSWSEIFELRGKYNNKNGTSNI-----ANNWYDSH 119
DB 92 VEEGENTLFFSSAPYTMGSAIO---NMFDERKRYER---FNTGPTAQWVMGHYVYVYRS 145
OY 120 DRKGAIVDC-----SGKTHVCOY--GPEAKGDGTYIEGAPCSGSDYAGVTCDDW 173
DB 146 YELGCAIAYCPDQPTKYVQVQCPGCGNHSRKYTPYSIGPPCGCPD-----ACD--- 197
OY 174 ONLTC 178
DB 198 -NGIC 201

RESULT 4
TPX1_HUMAN STANDARD; PRT; 243 AA.
ID TPX1_HUMAN
AC P16562;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Testis-specific protein TPX-1 precursor (Cysteine-rich secretory protein-2) (Crisp-2).
GN TPX1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90129048; PubMed=2613236;
RA Kusanaga M., Gutknecht J., Brew K., Spurr N., Goodfellow P.N.;
RT "Cloning and mapping of a testis-specific gene with sequence similarity to a sperm-coating glycoprotein gene.";
RL Eur. J. Biochem. 236:827-836(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96270732; PubMed=8665901;
RA Kraetzschmar J., Haendler B., Eberspacher U., Roostermann D.,
RT "The human cysteine-rich secretory protein (CRISP) family. Primary structure and tissue distribution of CRISP-1, CRISP-2 and CRISP-3.";
RL Eur. J. Biochem. 236:827-836(1996).
CC -1- SUBCELLULAR LOCATION: SECRETED (Probable).
CC -1- TISSUE SPECIFICITY: TESTIS AND EPIDIDYMIS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC -----
DR EMBL: M25532; AA61220.1; -;
DR EMBL: X95239; CA64526.1; -;
DR PIR: B33329; B33329.
DR Genbank: HGNC:12024; TPX1.
DR MIM: 187430; -;
DR InterPro: IPR001283; Allrgn_V5/TPX1.
DR Pfam: PF00188; SCP.1.
DR PRINTS: PRO0837; V5TPXLIKE.
DR ProDom: PD000542; Allrgn_V5/TPX1.1.

DR SMART: SMO0198; SCP.1.
DR PROSITE: PS01009; SCP_AGS_PRL_SC7_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRL_SC7_2; 1.
DR Testis; Signal; Multigene family.
FT SIGNAL 1 21
FT CHAIN 22 243
SQ SEQUENCE 243 AA; 27259 MW; CSFE698C449CFAD9 CRC64; 1.
Query Match 13.7%; Score 137; DB 1; Length 243;
Best Local Similarity 26.5%; Pred. No. 3e-05;
Matches 49; Conservative 28; Mismatches 72; Indels 36; Gaps 9;

OY 18 REMTEHLNGYBAFARARYKTSKRTVYDCTLEKAYSAKESDEPSEEE-----70
DB 38 REIYNK-HNELKRAVSP--PASNLMKEMREYTTAORMANKCTLOHSDPEDRKISTGC 94
OY 71 NVDYFSAATLNPLEAGNSWSEIFELRGKYNNKNGTSN-----IANNWYDSHDLGCA 125
DB 95 GENDLMSDPTSMSSHLSQWIDELDF--VIGVGRKSPNAVGHYQLWVSTYVQCG 151
OY 126 VVDC-----SGKTHVCOYGPPEAKGDGK--TYIEGAPCSGSDYAGVTCDD-----D 172
DB 152 IAYCPNDSLSKTYVCOYCPAGNNMNRKNTPTVQGTGCPACGPD-----DCDKGLCTNSQ 206
OY 173 WNLTL 177
DB 207 YQDL 211

RESULT 5
CRS3_HUMAN STANDARD; PRT; 245 AA.
ID CRS3_HUMAN
AC P54108; Q15512;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cysteine-rich secretory protein-3 precursor (CRISP-3) (SGP28 protein).
GN CRISP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96270732; PubMed=8665901;
RA Kraetzschmar J., Haendler B., Eberspacher U., Roostermann D.,
RT "The human cysteine-rich secretory protein (CRISP) family. Primary structure and tissue distribution of CRISP-1, CRISP-2 and CRISP-3.";
RL Eur. J. Biochem. 236:827-836(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96186934; PubMed=8601434;
RA Kjeldsen L., Cowland J.B., Johnson A.H., Borregaard N.;
RT "SGP28, a novel matrix glycoprotein in specific granules of human neutrophils with similarity to a human testis-specific gene product and a rodent sperm-coating glycoprotein.";
RL FEBS Lett. 380:246-250(1996).
CC -1- SUBCELLULAR LOCATION: SECRETED; IN NEUTROPHILS, LOCALIZED IN SPECIFIC GRANULES.
CC -1- TISSUE SPECIFICITY: SALIVARY GLAND, PANCREAS AND PROSTATE > EPIDIDYMIS, OVARY, THYMUS AND COLON.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC -----


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DR EMBL: X95240; CAA64527.1; -.
DR EMBL: X94323; CAA63984.1; -.
DR HSSP: P04284; ICPE.
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP.1.
DR PRINTS: PR00837; V5TPX1KE.
DR ProDom: PD00542; Allrgn_V5/Tpx1.
DR SMART: SM00198; SCP.1.
DR PROSITE: PS01009; SCP_AGS_PRL_SG7.1; 1.
DR PROSITE: PS01010; SCP_AGS_PRL_SG7.2; 1.
DR Glycoprotein; Signal; Multigene family; Polymorphism.
FT SIGNAL 1 20
FT CHAIN 1 245
FT CARBOHYD 239 239
FT VARIANT 106 106
FT VARIANT 134 134
SQ SEQUENCE 245 AA; 27630 MM; 84DD79CB7AE9E5F9 CRC64;
Query Match 13.5%; Score 135; DB 1; Length 245;
Best Local Similarity 25.1%; Pred. No. 4.6e-05;
Matches 48; Conservative 23; Mismatches 76; Indels 44; Gaps 8;
OY 14 DDDMEMETEL-----HNGYRAAF--ARNYKTSKRRTWYVCTLEEKAYK 56
DB 21 NEDKRPATLTALTTQYOVREIYNHNLRLRAVSPARN-----NLKKENKKEAANAQK 75
OY 57 SAEKCEEPSESEENADVFSATLTNIPLEANSWMSWSEIFELGKYNN-----KNG 106
DB 76 WANQCNWYHNSPNDRMTSLKQCE-NTLYSSASSWQAQNSWFDENINFDGCVGPKTPNA 134
OY 107 KTSNIANNWMSDSDXKGCNAVDCSC---KTHVYCOYGPEAGDQDKTI--YEGGAPRSC 160
DB 135 VVGHTVQVWYSSVLYGCGNACPRQKTKYYCYOCPRGAMNRLYPIEGAPCASC 194
OY 161 SPYGAAGTACD 171
DB 195 PD-----NCDD 200
RESULT 6
TPX1_MOUSE
ID TPX1_MOUSE STANDARD; PRT; 243 AA.
AC P16563;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Testis-specific protein TPX-1 precursor.
GN TPX1 OR TPX-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid:10090;
[1]
SEQUENCE FROM N.A.
RP
RN
RC TISSUE-Testis;
RX MEDLINE-90129048; PubMed-2613236;
RA Kasahara M., Gutknecht J., Brew K., Spurr N., Goodfellow P.N.;
RT Cloning and mapping of a testis-specific gene with sequence
RT similarity to a sperm-coating glycoprotein gene.";
RL Genomics 5:527-534(1989).
-1- SUPPLEMENTARY LOCATION: Secreted (Probable).
-1- TISSUE SPECIFICITY: TESTIS
-1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSICIS A63/A65; FUNGI SC7/SC14 AND PLANTS PR-1.
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CC
DR EMBL: M25533; AAA40472.1;
DR PIR: A33329; A33329.
DR MGG: P04284; 1CPE.
DR HSD; MGJ:98815; Tpx1.
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP_1.
DR PRINTS; PR00837; VSPFLIKE.
DR ProDom; PD000342; Allrgn_V5/Tpx1; 1.
DR SMART; SM00196; SCP_1.
DR PROSITE; PS01009; SCP_AGS_PRL_SCP_1; 1.
DR PROSITE; PS01010; SCP_AGS_PRL_SCP_2; 1.
RW Tests; Signal.
FT SIGNAL; 1 22
FT CHAIN; 23 243
SQ SEQUENCE 243 AA; 27605 MW; 6E07F569ACAA44 CRC64;

Query Match
Best local similarity 24.9%; Pred. No. 0.0024;
Matches 49; Conservative 28; Indels 36; Gaps 9

OY 11 ELDDDDKREFT-----ELHNGYRAAFARNYKSKMTFTVYDCTLEEKYSAEK 60
DB 21 ECKDDPDTSLFTNQLQVOREIYKKNELRSY--NPTGSDILKMKMSIOATYNAQKANK 78
OY 61 GSEPPSSSEENVVVFSAATLNPLEAGSMWSEFELFADKYNK-----GKTSNI- 112
DB 79 CILHSKDDR-KINRGENIYNSTDPITLSTVIG---SWNEHEDPYGVGAKPRSAV 134
OY 113 ----NMWSDHMDLGAAYVDCSGKHY---VGVGPEAKGCK--TYEGCAPCSRGD 162
DB 135 GHYQYLYVYSPFKIGCIATCNQDNKLTFFVCHYCPKMNMYMKSTFYQGCTPACASCR 194
OY 163 YGAYGTCD--DWQNL 177
DB 195 NCENGICNSCDFEDLL 211

RESULT 7
V45_POLD0 STANDARD; FRT; 206 AA.
AC P81656;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Venom allergen 5 (Antigen 5) (AG5) (Allergen Pol d 5).
OS Polistes dominulus (European paper wasp).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidea; Vespidae; Polietinae; Polistes.
OX NCBI_TaxID=34728;
RN [1]
RP SEQUENCE.
PC Tissue:Venom;
RA Hoffman D.R.;
RL Submitted (FEB-1999) to the SWISS-PROT data bank.
CC -!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG5/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
DR HSD; P04284; 1CPE.
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP_1.
DR PRINTS; PR00837; VSPFLIKE.
DR ProDom; PD000342; Allrgn_V5/Tpx1; 1.
DR SMART; SM00196; SCP_1.
DR PROSITE; PS01009; SCP_AGS_PRL_SCP_1; 1.
DR PROSITE; PS01010; SCP_AGS_PRL_SCP_2; 1.
RW Venom: Allergen.
FT DISULEID 4 16
FT DISULEID 8 104
FT DISULEID 28 96
FT DISULEID 172 189
SQ SEQUENCE 206 AA; 23152 MW; 2E325705A7875DAB CRC64;
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Query Match similarity      12.3%: Score 122.5; DB 1; Length 206;
Best Local Similarity      23.6%: Pred. No. 0.00049;
Matches      46; Conservative      32; Mismatches      70; Indels      47; Gaps      9;

OY      2 GDVSLCOOGE-----KL-----DDDRKFTLHNGYRAAFANRKT-----38
Db      11 GVHVCOYGESEKPEKNCAGKLKSYGPEEKEKLIYEHNRFQVAKGLGTYGNGPQO 70
OY      39 ---SKRTVYCYCTLEEKAYKSAEKSESPSESEENVDSAAITLNPLENGS-----89
Db      71 PAASNNMNLVWMDLAKIAQVMAQCOILIVHCKRHNKRYQAOV-NIAV-AGSSNHEPSV 128
OY      90 -----WMSBI--FELNRKYVNNK-KRTSNINAMWYDSHDKLKCAVVDGSGT---HVV 136
Db      129 TKLIQLENEVDVDFNYNTGITNKNRFRVGHYQVWMTXKVGCSGLKTYENQIHFL 188
OY      137 CGVGPFAKGDGKTY 151
Db      189 CNYGPAGNTIGOPT 203

RESULT 8
GILP_HUMAN
P48060.015409: STANDARD; PRT; 266 AA.
01-SEP-1996 (Rel. 33, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
G10ma pathogenesis-related protein (gilp) (RTVP-1 protein).
GILP OR RTVP1.
Homo sapiens (Human).
Mammalia; Eutheria; Chordata; Vertebrata; Euteleostomi;
Eumetazoa; Metazoa; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
[1]
RN      RP SEQUENCE FROM N.A.
RC      TISSUE-Glial tumor;
RA      MEDLINE=97128816; PubMed=8973356;
RX      Murphy E.V., Zhang Y., Zhu W., Blythe J.;
RT      "The human glioma pathogenesis-related protein is structurally
RT      related to plant pathogenesis-related proteins and its gene is
RT      expressed specifically in brain tumors.";
RN      RT Gene 1591131-135(1995).
[2]
RN      RP SEQUENCE OF 11-266 FROM N.A.
RC      TISSUE-Glial tumor;
RA      MEDLINE=9531646; PubMed=7607567;
RX      Murphy E.V., Zhang Y., Zhu W., Blythe J.;
RT      "The human glioma pathogenesis-related protein is structurally
RT      related to plant pathogenesis-related proteins and its gene is
RT      expressed specifically in brain tumors.";
RN      RT Gene 1591131-135(1995).
[3]
RN      RP STRUCTURE BY NMR
RC      MEDLINE=98151500; PubMed=9482873;
RX      Szepietowski T., Fernandez C., Mumenthaler C., Wuehrlich K.;
RT      "Structure comparison of human glioma pathogenesis-related protein
RT      GLIPR and the plant pathogenesis-related protein P1a indicates a
RT      functional link between the human immune system and a plant defense
RT      system.";
RN      RT Proc. Natl. Acad. Sci. U.S.A. 95:2262-2266(1998).
[4]
RN      RP TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE HUMAN BRAIN TUMOR,
RC      GLOBLASTOMA MULTIFORM/ASTROCYTOMA, BUT NEITHER IN NORMAL FETAL
CC      OR ADULT BRAIN TISSUE, NOR IN OTHER NERVOUS SYSTEM TUMORS.
[5]
RN      RP SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCF/TPX1;
CC      INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
[6]
RN      RP THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL: X91911; CAA63005.1; -
DR HSSP: U16307; AAA82731.1; -
DR HSSP: P04284; LCFE.
DR MIM: 602692; -
DR InterPro: IPR001283; Alltgn_V5/Tpx1.
DR Pfam: PF00188; SCP. 1.
DR PRINTS: PR00837; VSTPXLIKE.
DR ProDom: PD000542; Alltgn_V5/Tpx1; 1.
DR SMART: SMO0198; SCP. 1.
DR PROSITE: PS01009; SCP_AGS_PRL_SCT_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRL_SCT_2; 1.
DR CONFLICT 125 D->N (IN REF. 2)
FT FT 209 266
FC CONFLICT 209 266
SQ SEQUENCE 266 AA; 30342 MW; 343780B5EB2B7A CRC64;
      T (IN REF. 2)
Query Match          12.3%; Score 122; DB 1; Length 266;
Best Local Similarity 24.3%; Pred No 0.00074;
Matches 49; Conservative 30; Mismatches 68; Indels 50; Gaps 11
QY 14 DDDEKEMTELNHGVRARARARYKSKRMVYDCGLEEKAVKSSEK-----EEP-65
Db 30 NEDFIDKOCVRIHKHFSEVKPT--ASDMLVTWDPALAIARAKMSNCFSHNTLRKPH 87
QY 66 -----SEEN-----VOVFSAATNLPLEAGSNMSEI--FELRGVYKKNKTSNTIA 112
Db 88 KILHPFTSLGENTWTSVPDFSVSS-----ALTNWIDEIODDKRTICK--VCGHYT 139
QY 113 NNWVPSHKLCKCAVYDC-----SGRTHVCOYGPEAKGDGKT-IYEGACSCRSQD 162
Db 140 QYVMADSKYVCACAOECPKRVSGFDALNSGAIFICNTGP--GGNYTPWPYKRGCATCSACP 197
QY 163 YGAGVTCDDDMQNLLCI 179
Db 198 -----NDKCLDNLCY 207

RESULT 9
AEGI_MOUSE
ID AEGI_MOUSE STANDARD; PRT; 244 AA.
AC Q03401;
AC 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Spemc-coating glycoprotein 1 precursor (SCP 1) (acidic epidiymal
DE glycoprotein 1) (Cysteine-rich secretory protein-1) (Crisp-1).
GN AEGI OR AEG-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX NCBI_Taxid=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Submandibular gland;
RC MEDLINE=93246016; PubMed=101383;
RA Mizuki N.; Kasaiata M.;
RA "mouse submandibular glands express an androgen-regulated transcript
RT encoding an acidic epidiymal glycoprotein-like molecule";
RN MOL. CELL. ENDOCRINOI. 89:25-32(1992).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Submandibular gland;
RC MEDLINE=93307144; PubMed=831966;
RA Maendler R.; Krattschmar J.; Theuring F.; Schleuning W.D.; DE/AEG)
RT "transcript for cysteine-rich secretory protein-1 (CRISP-1; DE/AEG)
RT the mouse salivary gland.";
RC Endocrinology 133:192-198(1993).
CC -1. FUNCTION: THIS PROTEIN IS SUPPOSED TO HELP SPERMATOZOA UNDERGO
CC FUNCTIONAL MATURATION WHILE THEY MOVE FROM THE TESTIS TO THE
```

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CC DUCTUS DEFERENS.
CC -1 SUBCELLULAR LOCATION: STORED IN SECRETORY GRANULES OF GRANULAR
CC -1 CONVOLUTED TUBULES CELLS.
CC -1 TISSUE SPECIFICITY: MAINLY FOUND IN THE CAUDA EPIDIDYMAIS WHERE IT
CC IS SYNTHESIZED BY THE PRINCIPAL CELLS AND SECRETED INTO THE LUMEN.
CC BINDS TO THE HEADS OF SPERMATOZOA. ALSO EXPRESSED IN THE
CC SUBMANDIBULAR GLAND.
CC -1 DEVELOPMENTAL STAGE: EXPONENTIAL INCREASE BETWEEN DAYS 25 AND 30
CC AFTER BIRTH.
CC -1 INDUCTION: By androgens.
CC -1 SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M92849; AAA37185.1; -
DR EMBL: L05559; AAA37460.1; -
DR PIR: A49202; A49202.
DR MGJ: I02553; Aeg1.
DR InterPro: IPR001283; Allrgn_V5/7px1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR PRODOM: PD000542; Allrgn_V5/7px1; 1.
DR SMART: SM00198; SCP; 1.
DR PROSITE: PS01009; SCP_AGS_PRI_SC7_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRI_SC7_2; 1.
DR KMW: Glycoprotein; Signal.
DR SIGNAL: 1
DR CHAIN: 19
DR CARBOHYD: 20 244 N-LINKED (GLCNAC...) (POTENTIAL).
FT SEQUENCE 244 AA; 27679 MW; D0DD0348B857B1F CRC64;
SQ
Query Match 12.0%; Score 119.5; DB 1; Length 244;
Best Local Similarity 25.4%; Pred. No. 0.0011;
Matches 51; Conservative 31; Mismatches 84; Indels 35; Gaps 10;
OY 3 DYSICQOREKLD--DMREMFELHNGYRAFAFANKYTKSMRTVYDCTLEKAYKSAE 59
DB 21 DSSQENREKLEKSTKMSVQOEIVSKHQLRRVSPS--GSLDKMEMNYDAQVNAQWAD 78
OY 60 KCSEPSSESE-----ENVDFSAATLNIPLEAGNSMSEIFELRGKYNK--NGKT 108
DB 79 KCFSSHSPLELTNTNLRCGEN--LFMSYLAWSAIAQGVYNEKDLTYDVGPRQPSVY 136
OY 109 SNIANWYDSDHDKGCAVYDCSG--KTHVVGQGPPEAKGDGR--TITEGAPGCRGSDY 163
DB 137 GHYGVVWNSTFQVACGVACPKPRNRYYYCHICPVGNTGSLYTPYTAGSPCASCPDH 196
OY 164 GAGVVCDDDMNLIC---IGH 181
DB 197 -----CEDG---LCITNSGCH 208

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RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE-88124947; Pubmed-3422469;
RA Fang K.S.Y., Vitale M., Fehlner P., King T.P.;
RT "CDNA cloning and primary structure of a white-face hornet venom
RT allergen, antigen 5."
RL Proc. Natl. Acad. Sci. U.S.A. 85:895-899(1988).
RN [2]
RP PARTIAL SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE-Venom;
RX MEDLINE-90384920; Pubmed-2402482;
RA King T.P., Moran D., Wang D.F., Kochoumian L., Chalt B.T.;
RT "Structural studies of a hornet venom allergen antigen 5, Dol m v and
RT its sequence similarity with other proteins."
RL Protein Seq. Data Anal. 3:263-266(1990).
CC -1 SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC -----
DR EMBL: J03601; AAA28301.1; -
DR PIR: A31085; A31085.
DR HSSP: P04284; ICFE.
DR InterPro: IPR001283; Allrgn_V5/7px1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR PRODOM: PD000542; Allrgn_V5/7px1; 1.
DR SMART: SM00198; SCP; 1.
DR PROSITE: PS01009; SCP_AGS_PRI_SC7_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRI_SC7_2; 1.
DR KMW: Venom; Allergen; Signal; Multigene family.
DR SIGNAL: 1
DR CHAIN: 23
DR DISULFID: 24 227 VENOM ALLERGEN 5.01.
FT DISULFID 27 39
FT DISULFID 31 124
FT DISULFID 49 117
FT DISULFID 193 210
FT VARIANT 54 54 V -> A.
FT SEQUENCE 227 AA; 25999 MW; 4F0ED10D58C44502 CRC64;
SQ
Query Match 11.3%; Score 112.5; DB 1; Length 227;
Best Local Similarity 23.4%; Pred. No. 0.0043;
Matches 39; Conservative 27; Mismatches 74; Indels 27; Gaps 6;
OY 13 LDDDMREMFELHNGYRAFAFANKYTKSMRTVYDCTLEKAYKSAEKC- 61
DB 59 LNDENKEILAKRNDPRQNVAKGLETGRKGPQPPAKNNVLYWDELAKIAGTANQCD 118
OY 62 -----SEEPSSEENDVFS--NATLNIPLAGNSMSEIFELRGKYNK--KTS 109
DB 119 FNHDDCRNTAKYGVGNLMSITRTQFPDRSKLIRQWEDVETENKIKGLQNSNRKVG 178
OY 110 NIAMWYDSDHDKGCA--VYDCSGKH--VVCQYGPPEAKGDGKITYE 152
DB 179 HITQWVGKTRKELGCGSIXITIEDNMTYHLYVCNIGGNDENQPIYE 225

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RESULT 10
VAS2_DOLMA STANDARD; PRT; 227 AA.
AC P10736;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Venom allergen 5, 01 precursor (antigen 5 form 2) (AG5-2) (Allergen Dol
DE m 5.01) (Dol m V-A).
OS Dolichovespula maculata (White-face hornet) (Bald-faced hornet).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespidae; Vespinae; Dolichovespula.
NCBI_TaxID=7441;

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RESULT 11
VAS_VESGE STANDARD; PRT; 204 AA.
AC P35784;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Venom allergen 5 (antigen 5) (AG5) (Allergen Ves g 5) (Ves g V).
OS Vespula germanica (Yellow jacket) (Wasp).

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OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=30212;
RM [1]
RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=94044316; PubMed=8227862;
RA Hoffman D.R.;
RT "Allergens in Hymenoptera venom. XXV: The amino acid sequences of
RT antigen 5 molecules and the structural basis of antigenic cross-
RT reactivity."
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC PIR; H44522; H44522.
CC PIR; H44583; H44583.
CC HSSP; P04284; 1CFE.
CC InterPro; IPR001283; Allrgn_V5/TPx1.
CC Pfam; PF00188; SCP; 1.
CC PRINTS; PR00837; V5TPXLIKE.
CC PRODOM; PD000542; Allrgn_V5/TPx1.
CC SMART; SM00198; SCP; 1.
CC PROSITE; PS01009; SCP_AG5_PRL_SC7_1; 1.
CC PROSITE; PS01010; SCP_AG5_PRL_SC7_2; 1.
CC Venom; Allergen.
KW DISULFID 4 17 BY SIMILARITY.
FT DISULFID 8 101 BY SIMILARITY.
FT DISULFID 26 94 BY SIMILARITY.
FT DISULFID 170 187 BY SIMILARITY.
SQ SEQUENCE 204 AA; 23330 MW; D1F84BD21C7BCE CRC64;

Query Match 11.2%; Score 112; DB 1; Length 204;
Best local similarity 22.2%; Pred. No. 0.0042;
Matches 39; Conservative 34; Mismatches 69; Indels 34; Gaps 7;

OY 4 YELCOGRKLDHDDHREFTLHNGRAAFANRYT-----SKRTMYDCTLEEK 53
DB 34 YELTQGEKQ--DLIKE-----HNRKQKANGLETNGNPGOPPAKKNMNLWSDLAIT 86
OY 54 AKSKSEK-----SEPSSEENVDFSAATLNIPLLEAGNSWSEIFELR-GKTY 102
DB 87 AVMYMANQCGHGTCDHVKAFVGGVVALTSTAKTDNFKLVKMWDEKVDNPKRPF 146
OY 103 KNGN--KTSNIANNVWDSHDKLGA-----VDCSGKTHVCCGYGPEAKGDGRTIYE 152
DB 147 SENNELKIGHYTKVMANTRKVEGCSIKYIDDKMHHYLVCTGPGNGNEELYQ 202

RESULT 12
VAS2_VESCR STANDARD; PRT; 202 AA.
ID VAS2_VESCR
AC P35782;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Venom allergen 5.02 (Antigen 5-2) (AG5-2) (Allergen Vesp c 5.02) (Vesp
DE C.V.02).
OS Vespa crabro (European hornet).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7445;
RM [1]
RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=94044316; PubMed=8227862;
RA Hoffman D.R.;
RT "Allergens in Hymenoptera venom. XXV: The amino acid sequences of
RT antigen 5 molecules and the structural basis of antigenic cross-
RT reactivity."
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

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CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC PIR; H44522; H44522.
CC PIR; H44583; H44583.
CC HSSP; P04284; 1CFE.
CC InterPro; IPR001283; Allrgn_V5/TPx1.
CC Pfam; PF00188; SCP; 1.
CC PRINTS; PR00837; V5TPXLIKE.
CC PRODOM; PD000542; Allrgn_V5/TPx1.
CC SMART; SM00198; SCP; 1.
CC PROSITE; PS01009; SCP_AG5_PRL_SC7_1; 1.
CC PROSITE; PS01010; SCP_AG5_PRL_SC7_2; 1.
CC Venom; Allergen.
KW DISULFID 4 16 BY SIMILARITY.
FT DISULFID 8 101 BY SIMILARITY.
FT DISULFID 26 94 BY SIMILARITY.
FT DISULFID 168 185 BY SIMILARITY.
SQ SEQUENCE 202 AA; 22781 MW; B710E9198413F547 CRC64;

Query Match 11.2%; Score 111.5; DB 1; Length 202;
Best local similarity 22.8%; Pred. No. 0.0046;
Matches 37; Conservative 24; Mismatches 58; Indels 43; Gaps 5;

OY 25 HNGRYAFAFANRYT-----SKRTMYDCTLEEKAKSKSEK----- 61
DB 48 HNRKQKANGLETNGNPGOPPAKKNMNLWSDLAQIAQYMANQNGHDCRNSAKY 107
OY 62 -----SEPSSEENVDFSAATLNIPLLEAGNSWSEIFELR-GKYNNKGTSTNIANN 114
DB 108 SVGNINAGSTADNFVSNMVMK-----WEDEKVDGYGSPRNKLNKVGHYTM 158
OY 115 WDSHDKLGA-----VDCSGKTHVCCGYGPEAKGDGRTIYE 152
DB 159 VMATKEIGGSEDIYEDGMHRYLVCTGPGANGNEPIYE 200

RESULT 13
TPX1_CAVPO STANDARD; PRT; 244 AA.
ID TPX1_CAVPO
AC Q60477;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Testis-specific protein Tpx-1 precursor (Autoantigen 1) (25 kDa
DE acrosomal autoantigen) (AA1).
GN TPX1.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RM [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Hartley; TISSUE-Testis;
RX MEDLINE=96354287; PubMed=9115720;
RA Foster J.A.; Gerton G.L.;
RT "Autoantigen 1 of the guinea pig sperm acrosome is the homologue of
RT mouse Tpx-1 and human TPX1 and is a member of the cysteine-rich
RT secretory protein (CRISP) family."
RL Mol. Reprod. Dev. 44:221-229(1996).
RM [2]
RP SEQUENCE OF 22-41.
RX MEDLINE=88193219; PubMed=328255;
RA Hardy D.M.; Huang T.T.F.; Jr.; Driscoll W.J.; Tung K.S.K.; Wild G.C.;
RT "Purification and characterization of the primary acrosomal
RT autoantigen of guinea pig epididymal spermatozoa."
RL Biol. Reprod. 38:423-437(1988).
CC -1- TISSUE SPECIFICITY: TESTIS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

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[illegible]

SQ	SEQUENCE	206 AA;	23420 MW;	C269A4I0323A6DBE CRC64;
Oy	Query Match	11.1%;	Score 110.5;	DB 1; Length 206;
Db	Best Local Similarity	22.6%;	Pred. No. 0.0058;	
Matches	38;	Conservative	31;	Mismatches 72; Indels 27; Gaps 7;
Oy	13	I DDDMRREAFELINGRAAFANRKT-----SKMRVYDCLTEEKAYKSAKES	62	
Db	38	LTEMKEDELLKAVNDRPQVAMGLETSGNGPPQAPAKNNNNLVNMDELANIAQVAMSQCNC	97	
Oy	63	--EESSSEENDVY-----FSALLTNIPLEAGSMSEEFELRGCV--YKNKG--KTS	109	
Db	96	IGHDCIKTEKYEVGCGNIKAESTTIALLPDSFGKLVMKEMENKADNPPIETSKNNLTKTG	157	
Oy	110	NIANWYDSHDKLCA---VDSCGKTH-VYCOTGPBAKGDKITIEE	153	
Db	156	HYTGMVAKKTKETIGCGSVATYKADENTHTVLVCNIGPSNFNRNEKLYER	205	
RESULT 15				
VAS_VESSQ	STANDARD;	PRT;	205 AA.	
AC	P35786;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
De	Venom allergen 5 (Antigen 5) (AG5) (Allergen Ves s 5) (Ves s V).			
OC	Vespula squamosa (Southern yellow jacket) (Wasps).			
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;			
OC	Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;			
OC	Aculeata; Vespoidae; Vespidae; Vespinae; Vespula.			
RX	NCBI_Taxid=30214;			
RY	[1]			
RP	SEQUENCE.			
RC	TISSUE=Venom;			
RX	MEDLINE=94044316; PubMed=8227862;			
RA	Hoffman D.R.;			
RT	"Allergens in Hymenoptera venom. XXV. The amino acid sequences of			
RT	antigen 5 molecules and the structural basis of antigenic cross-			
RT	reactivity".			
J	Allergy Clin. Immunol. 92:707-716(1993)			
-1	SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPXI;			
CC	-1- SIMILARITY: AG3/AG5, FUNGI SC7/SCI4 AND PLANTS PR-1.			
RL				
CC				
DR	PIR; D45522; D44522.			
DR	PIR; D45834; D44583.			
DR	HSP; P04284; ICPE.			
DR	Interpro: IPROU1283; Allrgn_V5/Tpx1.			
DR	Pfam: PF00188; SCP: 1.			
DR	PRINTS; PR00837; VSTPLIKE.			
DR	Prodom: PD000542; Allrgn_V5/Tpx1; 1.			
DR	SMART; SMOU198; SCP: 1.			
DR	PROSITE; PS01009; SCP_AG5_PRI_SC7_1; 1.			
DR	PROSITE; PS01010; SCP_AG5_PRI_SC7_2; 1.			
VW	Venom; Allergen.			
FT	DISULFID 4 17 BY SIMILARITY.			
FT	DISULFID 8 102 BY SIMILARITY.			
FT	DISULFID 27 95 BY SIMILARITY.			
FT	DISULFID 171 188 BY SIMILARITY.			
SO	SEQUENCE 205 AA; 23114 MW; 8BB9C0DB6D44BA28 CRC64;			
Oy	Query Match	10.9%;	Score 108.5;	DB 1; Length 205;
Db	Best Local Similarity	23.3%;	Pred. No. 0.0086;	
Matches	38;	Conservative	29;	Mismatches 67; Indels 29; Gaps 7;
Oy	18	RMETTELHNTRYAAFAFRANKT-----SKMRVYDCLTEEKAYKSAKC-----	61	
Db	42	KOELIKITHDFRKVARGLFETGNNGPQAPAKNNNNLVNMDELANIAQVAMSQCNGHOT	101	
Oy	62	--SEPSSEENDVYSATSLNIPLEGNC---SWSEIFELAGKY--YKNKGTNSNIAN	113	
Db	102	CKDITTKIVGGINIAV--SSITAIVENNGLNYKAMENVDVDPPTISMEONEPFKTIIGHTO	160	
Oy	114	NWMDSHDKLCA---VDSCGKTH-VYCOTGPBAKGDKITIEE	152	

Db 161 MWAKTKKGGGSIKRYDNNMTHYLYVCNYPAGNFGNQEYVE 203

RESULT 16
ID VA53_DOLMA STANDARD: PRT: 215 AA.

AC P10737;
DE 01-JUL-1989 (Rel. 11, Created)
DE 01-JUN-1994 (Rel. 29, Last annotation update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE Venom allergen 5.02 precursor (Antigen 5 form 3) (AG5-3) (Allergen Dol m 5.02) (Dol m V-B) (Fragment).
DE m 5.02) (Dol m V-B) (Fragment).
DE Dolichovespula maculata (White-face hornet) (Bald-faced hornet).
DE Eukaryota; Metazoa; Arthropoda; Mandibulata; Hymenoptera; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidea; Vespidae; Vespine; Dolichovespula.
OX NCBI_TaxID=7441;
[1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=88124947; PubMed=3422469;
RA Fung K.S.Y., Vitale M., Rehner P., King T.P.;
RT "CDNA cloning and primary structure of a white-face hornet venom allergen, antigen 5.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:895-899(1988).
[2]
RN PARTIAL SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE-Venom;
RX MEDLINE=90384920; PubMed=2402482;
RA King T.P., Moran D., Wang D.P., Kochoumian L., Chait B.T.;
RT "Structural studies of a hornet venom allergen antigen 5, Dol m V and its sequence similarity with other proteins.";
RL Protein Seq. Data Anal. 3:263-266(1990).
[3]
CC -1 SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC -----
DR EMBL: J03602; AAA28302.1; ALT_TERM.
DR PIR: B31085; B31085.
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP. 1.
DR ProDom: PD000542; Allrgn_V5/Tpx1. 1.
DR SMART: SM00198; SCP. 1.
DR PROSITE: PS01009; SCP AG5_PRL SC7.1; 1.
DR PROSITE: PS01010; SCP AG5_PRL SC7.2; 1.
KW Venom; Allergen; Signal; Multigene family.
FT NON_TER 1
FT SIGNAL 1
FT CHAIN 1
FT DISULFID 11 215 VENOM ALLERGEN 5.02.
FT DISULFID 14 26
FT DISULFID 18 111
FT DISULFID 36 104
FT DISULFID 183 198
SQ SEQUENCE 215 AA; 24270 MW; D8FEEB99CE9A0BA CRC64;

Query Match 10.8%; Score 108; DB 1; Length 215;
Best Local Similarity 23.4%; Pred. No. 0.01;
Matches 40; Conservative 30; Mismatches 67; Indels 34; Gaps 8;

Qy 13 LDDMKEMFELHNGYGAFAARNYKT-----SKMTVYDCTLEKAKYSAEKCS 62
Db 46 VSNDEKNETVNRHNOFQKAVKGLFTRGNPGPOPAKRNMYLVNDELAKRIQOTVANCOS 105

Qy 63 -----EPPSSEENVDFSA-----ATLNIPLGNSWSEIFEL---NGKYNNRN 105
Db 131 -----DCPSDCDNGIC 141

Db 106 FCHDCKRTEKYOYGVONVALASTGNSYATWSKLIB---MWENEKDFNPAGTMDNNF 162

Qy 106 GRTSNIANMWVDSHDKLCA---VYDCSGKTH-VVCOYGPBKAQGGRTIVE 152
Db 163 SKVGHYTOVMWAGTKKKEIGGSVKYIENNMTHTLYVCNYPAGNMYMDQYIYE 213

RESULT 17
ID CRVP_TRIM STANDARD: PRT: 163 AA.

AC P79845;
DE 01-NOV-1997 (Rel. 35, Created)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cysteine-rich venom protein precursor (CRVP).
DE Trimeresurus mucrosquamatus (Taiwan habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubridae;
OC Viperidae; Crotalinae; Protobothrops.
OX NCBI_TaxID=103944;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE-Venom gland;
RX MEDLINE=97385768; PubMed=9241782;
RA Chang T.-Y., Mao S.-H., Guo Y.-W.;
RT Cloning and expression of a cysteine-rich venom protein from Trimeresurus mucrosquamatus (Taiwan habu)."
RL Toxicon 35:879-888(1997).
[2]
CC -1 FUNCTION: May be a toxin that blocks ryanodine receptors.
CC -1 SUBCELLULAR LOCATION: Secreted.
CC -1 TISSUE SPECIFICITY: Produced by the venomous gland.
CC -1 SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC -----
DR EMBL: U59447; AAB48565.1;
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP. 1.
DR PRINTS: PR00837; VSTPLIKE.
DR ProDom: PD000542; Allrgn_V5/Tpx1. 1.
DR SMART: SM00198; SCP. 1.
DR PROSITE: PS01009; SCP AG5_PRL SC7.1; 1.
DR PROSITE: PS01010; SCP AG5_PRL SC7.2; 1.
KW Calcium channel inhibitor; Neotoxin; Toxin; Signal.
FT CHAIN 22
FT SIGNAL 21
FT CHAIN 183
SQ SEQUENCE 183 AA; 20378 MW; 50224D8E92A64930 CRC64;

Query Match 10.7%; Score 107; DB 1; Length 183;
Best Local Similarity 27.1%; Pred. No. 0.01;
Matches 38; Conservative 12; Mismatches 66; Indels 24; Gaps 5;

Qy 54 AYKSAKCESEPPSSEENVDFSAATINIPLEAGNSWSEIF-----ELRGKYNN----- 103
Db 11 AERNAYRCISHSRSRSRYLIGIKGCEITVMSYPAKWDIIHANHGKXKFGVGAAP 70

Qy 104 KNGRTSNIANMWVDSHDKLCAVYDCSGKTH---VVCQYGPBKAQGGRTI---YEEGAPCS 158
Db 71 SNAATGHTYTOIIVYKRSYRGCCAAVCPSSKRYFYCYQCPAGNMGICHTAPYTSPPCG 130

Qy 159 RCDYAGVATCDDDMONLILC 178
Db 131 -----DCPSDCDNGIC 141

RESULT 18

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VA5_VESMC          STANDARD;          PRT:          204 AA.
ID VAS1_VESMC
AC P35760;
RT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
OS Venom allergen 5 (Antigen 5) (AG5) (Allergen Ves m 5) (Ves m V).
OC Vesputia maculifrons (Eastern yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidea; Vespidae; Vespinae; Vesputia.
OX NCBI_TaxID=7453;
RN [1]
RP SEQUENCE.
RC MEDLINE=93203603; PubMed=8454859;
RA La G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;
RT "Sequence analysis and antigenic cross-reactivity of a venom
RT allergen, antigen 5, from hornets, wasps, and yellow jackets."
RL J. Immunol. 150:2823-2830(1993).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
DR HSSP; P04284; ICPE.
DR InterPro; IPR001283; Allrgn_V5/TPx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPXLIKE.
DR PRODOM; PD000542; Allrgn_V5/TPx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; SCP_AGS_Prl_Sc7_1; 1.
DR PROSITE; PS01010; SCP_AGS_Prl_Sc7_2; 1.
KM Venom; Allergen.
FT DISULFID 4 17 BY SIMILARITY.
FT DISULFID 8 101 BY SIMILARITY.
FT DISULFID 26 94 BY SIMILARITY.
FT DISULFID 170 187 BY SIMILARITY.
SQ SEQUENCE 204 AA; 23332 MW; 8B68A94C1390311 CRC64;

Query Match 10.7%; Score 107; DB 1; Length 204;
Best Local Similarity 21.6%; Pred. No. 0.012; Mismatches 34; Gaps 7;
Matches 38; Conservative 34; Indels 34;

QY 4 YSLCQREKLDMDMEFTLHNGYRAAFARNTK-----SKMRTVYDCTLEEK 53
ID VAS1_VESCR          STANDARD;          PRT:          204 AA.
AC P35781;
RT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
OS Venom allergen 5 (Antigen 5) (AG5) (Allergen Ves f 5) (Ves f V).
OC Vesputia flavopilosa (Yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidea; Vespidae; Vespinae; Vesputia.
OX NCBI_TaxID=30211;
RN [1]
RP SEQUENCE.
RC MEDLINE=94044316; PubMed=8227862;
RA Hoffman D.R.;
RT "Allergens in Hymenoptera venom, XXV: The amino acid sequences of
RT antigen 5 molecules and the structural basis of antigenic cross-
RT reactivity."
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -1- FUNCTION: MAY HAVE AN ANCESTRAL FUNCTION IN THE PROMOTION OF
CC OVUM FERTILIZATION BY Sperm.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
DR HSSP; P04284; ICPE.
DR InterPro; IPR001283; Allrgn_V5/TPx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPXLIKE.
DR PRODOM; PD000542; Allrgn_V5/TPx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; SCP_AGS_Prl_Sc7_1; 1.
DR PROSITE; PS01010; SCP_AGS_Prl_Sc7_2; 1.
KM Venom; Allergen.
FT DISULFID 4 17 BY SIMILARITY.
FT DISULFID 8 101 BY SIMILARITY.
FT DISULFID 26 94 BY SIMILARITY.
FT DISULFID 170 187 BY SIMILARITY.
SQ SEQUENCE 204 AA; 23274 MW; 7667232536A32FC5 CRC64;

Query Match 10.6%; Score 106; DB 1; Length 204;
Best Local Similarity 21.6%; Pred. No. 0.014; Mismatches 36; Gaps 7;
Matches 38; Conservative 35; Indels 34;

QY 4 YSLCQREKLDMDMEFTLHNGYRAAFARNTK-----SKMRTVYDCTLEEK 53
ID VAS1_VESCR          STANDARD;          PRT:          202 AA.
AC P35781;
RT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
OS Venom allergen 5.01 (Antigen 5-1) (AG5-1) (Allergen Ves c 5.01) (Ves
DE c V.01).
OC Vespa crotto (European hornet).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7445;
RN [1]
RP SEQUENCE.
RC MEDLINE=94044316; PubMed=8227862;
RA Hoffman D.R.;
RT "Allergens in Hymenoptera venom, XXV: The amino acid sequences of
RT antigen 5 molecules and the structural basis of antigenic cross-
RT reactivity."
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
DR HSSP; P04284; ICPE.
DR InterPro; IPR001283; Allrgn_V5/TPx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPXLIKE.

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RT "Allergens in Hymenoptera venom, XXV: The amino acid sequences of
RT antigen 5 molecules and the structural basis of antigenic cross-
RT reactivity."
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -1- FUNCTION: MAY HAVE AN ANCESTRAL FUNCTION IN THE PROMOTION OF
CC OVUM FERTILIZATION BY Sperm.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
DR HSSP; P04284; ICPE.
DR InterPro; IPR001283; Allrgn_V5/TPx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPXLIKE.
DR PRODOM; PD000542; Allrgn_V5/TPx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; SCP_AGS_Prl_Sc7_1; 1.
DR PROSITE; PS01010; SCP_AGS_Prl_Sc7_2; 1.
KM Venom; Allergen.
FT DISULFID 4 17 BY SIMILARITY.
FT DISULFID 8 101 BY SIMILARITY.
FT DISULFID 26 94 BY SIMILARITY.
FT DISULFID 170 187 BY SIMILARITY.
SQ SEQUENCE 204 AA; 23274 MW; 7667232536A32FC5 CRC64;

Query Match 10.6%; Score 106; DB 1; Length 204;
Best Local Similarity 21.6%; Pred. No. 0.014; Mismatches 36; Gaps 7;
Matches 38; Conservative 35; Indels 34;

QY 4 YSLCQREKLDMDMEFTLHNGYRAAFARNTK-----SKMRTVYDCTLEEK 53
ID VAS1_VESCR          STANDARD;          PRT:          202 AA.
AC P35781;
RT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
OS Venom allergen 5.01 (Antigen 5-1) (AG5-1) (Allergen Ves c 5.01) (Ves
DE c V.01).
OC Vespa crotto (European hornet).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7445;
RN [1]
RP SEQUENCE.
RC MEDLINE=94044316; PubMed=8227862;
RA Hoffman D.R.;
RT "Allergens in Hymenoptera venom, XXV: The amino acid sequences of
RT antigen 5 molecules and the structural basis of antigenic cross-
RT reactivity."
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
DR HSSP; P04284; ICPE.
DR InterPro; IPR001283; Allrgn_V5/TPx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPXLIKE.

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DR PRODOM: PD000542; Allrgn_V5/Tpx1; 1.
 DR SMART: SM00198; SCP; 1.
 DR PROSITE: PS01009; SCP_AGS_PRI_SCT_1; 1.
 DR PROSITE: PS01010; SCP_AGS_PRI_SCT_2; 1.
 KW Venom: Allergen.
 FT DISULFID 4 16 BY SIMILARITY.
 FT DISULFID 8 101 BY SIMILARITY.
 FT DISULFID 26 94 BY SIMILARITY.
 FT DISULFID 168 185 BY SIMILARITY.
 SQ SEQUENCE 202 AA; 22722 MW; EDEB39905B598997 CRC64;
 Query Match 10.6%; Score 105.5; DB 1; Length 202;
 Best Local Similarity 22.2%; Pred. No. 0.016;
 Matches 35; Conservative 26; Mismatches 62; Indels 35; Gaps 6;
 QY 25 HNGYRAAFARNTKT-----SKARTMYDCTLEKAKYSAKCS-----62
 DB 48 HNEFRKQVARGLETGNFGPQPPAKSMNTLVNDELADIAQVMAVNCNGHDCNRSAXY 107
 QY 63 ---EEPSSEENVDFSAATLNIPLRAGNSWSEIFELR-GKYVKNKGTSTNIAWVDS 118
 DB 108 SVGQNTAEGSTADNFSGVSNMVKM-----WDEKDYQYSGPKNKLNKGYTQVWAK 162
 QY 119 HDKLGCAVDC--SG--KTHVCCQYGPPEAKGDKRTYE 152
 DB 163 TKEIGSGSTIKYIENGMRHRYLVACNYPGAGVNGEPIYE 200
 RESULT 21
 ID YRBL_CAEEL STANDARD: PRT; 312 AA.
 AC 009366; (rel. 35; Created).
 DT 01-NOV-1997 (rel. 35; Last sequence update).
 DT 16-NOV-2001 (rel. 40; Last annotation update).
 DT 16-NOV-2001 (rel. 40; Last annotation update).
 GN Hypothetical 35.0 kDa protein F48E8.1 in chromosome III.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditidae; Rhabditioidea;
 OC Rhabditidae; Polodeirinae; Caenorhabditis.
 NCBI_TaxID=6239;
 RN NCI
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Kirsten J.;
 RT Submitted (MAR-1995) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
 CC -1- INSECTS AG3/AG5; FUNGI SCT/SC14 AND PLANTS PR-1.
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL; U23514; AAC46538.1;
 DR WormPep; F48E8.1; CE01953.
 DR InterPro; IPR001283; Allrgn_V5/Tpx1.
 DR Pfam; PF00188; SCP; 1.
 DR PRINTS; PR00837; V5TPXLIKE.
 DR PRODOM; PD000542; Allrgn_V5/Tpx1; 1.
 DR SMART; SM00198; SCP; 1.
 DR PROSITE; PS01009; SCP_AGS_PRI_SCT_1; FALSE_NEG.
 DR PROSITE; PS01010; SCP_AGS_PRI_SCT_2; FALSE_NEG.
 KW Hypothetical protein.
 FT DOMAIN 265 268 POLY-THR.
 FT DOMAIN 299 303 POLY-GLU.
 SQ SEQUENCE 312 AA; 35054 MW; AEFCTBFF25E26288 CRC64;
 Query Match 10.5%; Score 105; DB 1; Length 312;
 Best Local Similarity 21.7%; Pred. No. 0.029;

Matches 41; Conservative 30; Mismatches 80; Indels 38; Gaps 8;
 QY 1 EDDVSLCOQREKLDMDRMFEELINGYRAAFARNTKSTKRTMYDCTLEKAKYSAK 60
 DB 64 QSDSGLSRSRSHENRYLKWITHEHNRFR---RMVPASDMNKLWSEDLASQRIADT 119
 QY 61 CSEEPSSEENV--DYFSAATLNIPLRAGNSWSEIFELR-GKYVKNKGTSTNIAWVDS 117
 DB 120 CDFRSRGRINVENTNIAAPYSNYS-DAISITFENEHNPCCGNHAYHCCGHVQVWA 178
 QY 118 SHDKLGCAVDCS-----GKTH---VVCYGPPEAKGDKRTYE-----151
 DB 179 KTNLVGCGCFRCHDVGQVWGRHNRVFCYHNPQ---GNTVFYTAQOLYAMFAFTWAS 234
 QY 152 EEGAPCSRC 160
 DB 235 GDNGKCSNC 243
 RESULT 22
 ID VAS_VESPE STANDARD: PRT; 204 AA.
 AC P33785;
 DT 01-JUN-1994 (rel. 29; Created).
 DT 01-NOV-1997 (rel. 35; Last sequence update).
 DT 01-NOV-1997 (rel. 35; Last annotation update).
 DT 01-NOV-1997 (rel. 35; Last annotation update).
 GN Venom allergen 5 (Allergen 5) (AG5) (Allergen Yes p 5) (Yes p V).
 OS Vespaula pensylvanica (American yellow jacket) (Maep).
 OS Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Vespidae; Neoptera; Endopterygota; Hymenoptera; Apocrita;
 OC Hymenoptera; Vespidae; Vespidae; Vespidae; Vespidae; Vespidae;
 NCBI_TaxID=30213;
 RN NCI
 RP SEQUENCE.
 RC TISSUE-Venom;
 RX MEDLINE=94044316; PubMed=8227862;
 RA Hoffman D.R.;
 RT "Allergens in Hymenoptera venom. XXV: The amino acid sequences of
 RT antigen 5 molecules and the structural basis of antigenic cross-
 RT reactivity".
 RT J. Allergy Clin. Immunol. 92:707-716(1993).
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
 CC -1- INSECTS AG3/AG5; FUNGI SCT/SC14 AND PLANTS PR-1.
 CC PIR; C44522; C44522.
 DR PIR; C44583; C44583.
 DR HSSP; P04284; ICFE.
 DR InterPro; IPR001283; Allrgn_V5/Tpx1.
 DR Pfam; PF00188; SCP; 1.
 DR PRINTS; PR00837; V5TPXLIKE.
 DR PRODOM; PD000542; Allrgn_V5/Tpx1; 1.
 DR SMART; SM00198; SCP; 1.
 DR PROSITE; PS01009; SCP_AGS_PRI_SCT_1; 1.
 DR PROSITE; PS01010; SCP_AGS_PRI_SCT_2; 1.
 KW Venom: Allergen.
 FT DISULFID 4 17 BY SIMILARITY.
 FT DISULFID 8 101 BY SIMILARITY.
 FT DISULFID 26 94 BY SIMILARITY.
 FT DISULFID 170 187 BY SIMILARITY.
 SQ SEQUENCE 204 AA; 23317 MW; 85ED971066C/D7C8 CRC64;
 Query Match 10.3%; Score 103; DB 1; Length 204;
 Best Local Similarity 20.6%; Pred. No. 0.027;
 Matches 35; Conservative 31; Mismatches 72; Indels 32; Gaps 5;
 QY 10 REKLDDMEKFEELINGYRAAFARNTKT-----SKARTMYDCTLEKAKYSAK 59
 DB 38 KEKKDILKE-----HNEFRKQVARGLETGNFGPQPPAKSMNTLVNDELAVYQVWAK 92
 QY 60 KC-----SEEPSSEENVDFSAATLNIPLRAGNSWSEIFELR---VYKNG 106
 DB 93 QCYGHDTCRDVAKIPGVQNVALGSGADKIDNPVKLYKMEDEVADYPAKPKSENNFN 152
 QY 107 KTSNIAWVDSHDKLGCAVDCS-----GKTHVCCQYGPPEAKGDKRTYE 152


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Db      153 KIGHTOMWANTKEIGCGSIKTYIONEMKHYLVCONYPSGNGFNELTYQ 202
RESULT 23
ID      VA5_VESVU      STANDARD;      PRT;      227 AA.
AC      Q05110; Q9UB91;
DT      01-FEB-1994 (Rel. 28, Created)
DT      01-FEB-1994 (Rel. 28, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Venom allergen 5 precursor (Antigen 5) (AG5) (Allergen Ves v 5) (Ves v
V).
OS      Vesipula vulgaris (Yellow Jacket) (Masp).
OC      Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC      Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC      Aculeata; Vespoidea; Vespidae; Vespinae; Vespula.
OX      NCBI_TaxID=7454;
RN      [1]
RP      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC      TISSUE=Venom;
RX      MEDLINE=93203603; PubMed=8454859;
RA      Lu G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;
RT      "Sequence analysis and antigenic cross-reactivity of a venom
allergen, antigen 5, from hornets, wasps, and yellow jackets.";
RL      J. Immunol. 150:2823-2830(1993).
RN      [2]
RP      SEQUENCE OF 24-227 FROM N.A.
RA      Suck R., Hagen S., Piebig H.;
RT      "Molecular cloning of a genomic sequence from the venom allergen
allergen 5 from Vesipula vulgaris.";
RL      Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC      -1- INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC      -----
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CC      -----
DR      EMBL; M98858; AAA30333.1;
DR      EMBL; AJ38849; CAB42887.1;
DR      HSSP; P04284; ICPE.
DR      InterPro; IPR001283; Allrgn_V5/TPx1.
DR      Pfam; PF00188; SCP.1.
DR      PRINTS; PR00837; V5TPX1KE.
DR      PRODOM; PD000542; Allrgn_V5/TPx1.1.
DR      SMART; SM00198; SCP.1.
DR      PROSITE; PS01009; SCP_AGS_PRL_SCT_1; 1.
DR      PROSITE; PS01010; SCP_AGS_PRL_SCT_2; 1.
KW      Venom; Allergen; signal.
FT      SIGNAL      1      23
FT      CHAIN      24      227
FT      DISULFID      27      40
FT      DISULFID      31      124
FT      DISULFID      49      117
FT      DISULFID      193      210
FT      CONFLICT      109      109
FT      CONFLICT      118      118
FT      CONFLICT      173      173
FT      CONFLICT      219      219
SQ      SEQUENCE      227 AA; 25798 MM; 999813740A66F55 CMC64;
Query Match      10 38; Score 103; DB 1; Length 227;
Best Local Similarity 21.58; Pred No. 0.03;
Matches 39; Conservative 32; Mismatches 66; Indels 44; Gaps 7;
OY      4 YSLCOORELDDMKEFTELHNGYRAARARIKT-----SKARTMYDCTLEEK 53
Db      57 YGLTKDEKO-DLKE-----HNDPFOKTKARGLTRGNPFGPPAKMKMLVNDLAV 109

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OY      54 AYKSAKNC-----SEEPSSEENVDFSAATLNIPLDAGNSWSEIFELRGKVN 103
Db      110 AQVWANDCOYGHDTCDVAKYQVGNVALTGSTARKYDQDPVXLVIMDEEV-----KDVN 164
OY      104 KNG-----KTSNIANNVMDSHDKLQCA-----VYDCSGKTHVVCQYPRANKDGKTY 151
Db      165 PKRKSFGNDFLKTGYTQVWANTKEVCGSIKTYOEMKHYLVCONYPSGNGFNELTY 224
OY      152 E 152
Db      225 Q 225
RESULT 24
AGS2_MOUSE
ID      AGS2_MOUSE      STANDARD;      PRT;      241 AA.
AC      Q03402;
DT      01-OCT-1993 (Rel. 27, Created)
DT      01-OCT-1993 (Rel. 27, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Sperm-coating glycoprotein 2 precursor (SCP 2) (Acidic epididymal
glycoprotein 2) (Cysteine-rich secretory protein-3) (Crisp-3).
CN      AGS2 OR AGS-2
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Submandibular gland;
RX      MEDLINE=93246016; PubMed=1501383;
RA      Mizuki N., Kasahara M.;
RT      "Mouse submandibular glands express an androgen-regulated transcript
encoding an acidic epididymal glycoprotein-like molecule.";
RL      Mol. Cell. Endocrinol. 89:25-32(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Submandibular gland;
RX      MEDLINE=93307144; PubMed=8319566;
RA      Haendler B., Kretzschmar J., Theuring F., Schlenning W.D.;
RT      "Transcripts for cysteine-rich secretory protein-1 (CRISP-1, DE/AGS)
and the novel related CRISP-3 are expressed under androgen control in
the mouse salivary gland.";
RL      Endocrinology 133:192-198(1993).
CC      -1- FUNCTION: THIS PROTEIN IS SUPPOSED TO HELP SPERMATOZOON UNDERGO
FUNCTIONAL MATURATION WHILE THEY MOVE FROM THE TESTIS TO THE
DUCTUS DEFERENS.
CC      -1- SUBCELLULAR LOCATION: STORED IN SECRETORY GRANULES OF GRANULAR
CONVOLUTED TUBULES CELLS.
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN SUBMANDIBULAR GLAND.
CC      -1- DEVELOPMENTAL STAGE: EXPONENTIAL INCREASE BETWEEN DAYS 25 AND 30
AFTER BIRTH.
CC      -1- INDUCTION: By androgens.
CC      -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC      -----
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CC      -----
DR      EMBL; M92850; AAA37186.1;
DR      EMBL; I05560; AAA37461.1;
DR      PIR; B49202; B49202.
DR      MGI; MGI:102552; Ags2.
DR      InterPro; IPR001283; Allrgn_V5/TPx1.
DR      Pfam; PF00188; SCP.1.
DR      PRINTS; PR00837; V5TPX1KE.
DR      PRODOM; PD000542; Allrgn_V5/TPx1.1.

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DR SMART: SM00198; SCP: 1.
 DR PROSITE: PS01009; SCP_AGS_PRL_SC7_1; 1.
 DR PROSITE: PS01010; SCP_AGS_PRL_SC7_2; 1.
 DR Sperm: Glycoprotein; Signal.
 FT SGNL 1 19
 FT CHAIN 20 241
 FT CARBOHYD 118 118 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 132 132 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 175 175 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 241 AA: 27314 MW, D903788BAE4001BF CRC64;
 Query Match 10.1%; Score 101; DB 1; Length 241;
 Best Local Similarity 23.3%; Pred. No. 0.049;
 Matches 45; Conservative 31; Mismatches 67; Indels 50; Gaps 12;
 QY 11 ERLDDHREMTTEL--HNGYRAFAFARYKSKRTMYVDCLEERAKYSAKCEPSS 67
 DB 29 ERLSTSKSKSYOEELVSKHNLKRYKSPS--GSDLLNENNYDAQVNAQDRDKTFESHSP 86
 QY 68 EE-----ENVDFSAATINIPLEAGNSWSEIF-----ELGKRYNNKNGTSHIA- 112
 DB 87 IELRTNLRKGEN--LFSSTYL-VP-----SSVYQGYTESKGLIFGV-GPKQWASY 135
 QY 113 -----NMWDSHDKCAVVDGSG---KTHVCCGYGPEAKGDK-----TITYEGAPCS 158
 DB 136 VGHRTQVYVMSNLDQACGVAECPEPNLRYFYVCRTCLVNTSGHYPSRPLATYARAPCA 195
 QY 159 RGSYDGAQVTCDD 171
 DB 196 SCPD-----RCED 203
 RESULT 25
 VAS_DOLAR STANDARD; PRT; 203 AA.
 ID VAS_DOLAR
 AC 005108;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Venom allergen 5 (Antigen 5) (AG5) (Allergen Dol a 5) (Dol a V).
 OS Dolichovespula arenaria (Yellow hornet).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
 OC Aculeata; Vespoidea; Vespidae; Vespinae; Dolichovespula.
 NC NCB1_TaxID=7442;
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=93203603; PubMed=8454859;
 RA Lu G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;
 RT "Sequence analysis and antigenic cross-reactivity of a venom
 allergen, antigen 5, from hornets, wasps, and yellow jackets.";
 RL J. Immunol. 150:2823-2830(1993).
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
 CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
 CC
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 CC
 CC EMBL: M98859; AAA28303.1;
 DR HSSP: P04284; ICPE.
 DR InterPro: IPR001283; ALLrgn_V5/TPX1.
 DR Pfam: PF00188; SCP; 1.
 DR PRINTS: PRO0837; V5TPXLIKE.
 DR PRODOM: PD000542; ALLrgn_V5/TPX1; 1.
 DR SMART: SM00198; SCP; 1.
 DR PROSITE: PS01009; SCP_AGS_PRL_SC7_1; 1.
 DR PROSITE: PS01010; SCP_AGS_PRL_SC7_2; 1.

KW Venom: Allergen.
 FT DISULFID 4 15 BY SIMILARITY.
 FT DISULFID 7 100 BY SIMILARITY.
 FT DISULFID 25 93 BY SIMILARITY.
 FT DISULFID 169 186 BY SIMILARITY.
 SQ SEQUENCE 203 AA: 23202 MW, 6D5C725AD4EBC4B CRC64;
 Query Match 10.1%; Score 100.5; DB 1; Length 203;
 Best Local Similarity 19.2%; Pred. No. 0.044;
 Matches 37; Conservative 31; Mismatches 84; Indels 41; Gaps 6;
 QY 1 EGYSLCQRETL-----DDMRMTTELHNGYRAFAFARYKT----- 38
 DB 9 KGHITLCKGTSMKNCCKGKLYKSYGVYNDKNEYKHNFEKQVAGLRTGNRGP 68
 QY 39 --SKARTYVDCLEERAKYSAKCEPSSSEBNDVFSATLNIPLEAGNS----- 89
 DB 69 PAKNNMLVWDELAKIKQVWANCNFGHDQCRNTAKYPGQNVALASTGNSYOTMSYL 128
 QY 90 ---WSEIFEL--RGKYNNKNGTSHIANWYDSDHRLGCA--VYDSCGKTH-VGQY 139
 DB 129 IKMDEVDKYNPHKDLNHNFSKVGHYQWVGKTEIGGSVYKLNKMHYLYCNY 188
 QY 140 GPEAKGDKTYE 152
 DB 189 GPAGNTWNPVYE 201
 RESULT 26
 PRLA_LYCSES STANDARD; PRT; 175 AA.
 ID PRLA_LYCSES
 AC 008697;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Pathogenesis-related protein 1A1 precursor (PR-1A1).
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 NC NCB1_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Rutgers; TISSUE=leaf;
 RX MEDLINE=94247356; PubMed=8190070;
 RA Torniero P., Conejero V., Vera P.;
 RT "A gene encoding a novel isoform of the PR-1 protein family from
 tomato is induced upon viral infection.";
 RL Mol. Gen. Genet. 243:47-53(1994).
 CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
 CC AGAINST PATHOGENS (BY SIMILARITY)
 CC -1- INDUCTION: SYNTHESIZED DURING PATHOGEN INFECTION OR OTHER STRESS-
 CC RELATED RESPONSES.
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
 CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
 CC
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 CC
 CC EMBL: X71592; CA505956.1;
 DR HSSP: P04284; ICPE.
 DR InterPro: IPR001283; ALLrgn_V5/TPX1.
 DR Pfam: PF00188; SCP; 1.
 DR PRINTS: PRO0837; V5TPXLIKE.
 DR PRODOM: PD000542; ALLrgn_V5/TPX1; 1.
 DR SMART: SM00198; SCP; 1.
 DR PROSITE: PS01009; SCP_AGS_PRL_SC7_1; 1.
 DR PROSITE: PS01010; SCP_AGS_PRL_SC7_2; 1.

KW Plant defense; Pathogenesis-related protein; Signal; Multigene family.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 175 PATHOGENESIS-RELATED PROTEIN 1A1.
 FT DISULFID 65 135 BY SIMILARITY.
 FT DISULFID 108 114 BY SIMILARITY.
 FT DISULFID 130 144 BY SIMILARITY.
 SQ SEQUENCE 175 AA; 19660 MW; 0DF68E9062FAC1 CRC64;
 Query Match 9.6%; Score 96; DB 1; Length 175;
 Best Local Similarity 26.4%; Pred. No. 0.093;
 Matches 39; Conservative 13; Mismatches 48; Indels 48; Gaps 8;
 OY 18 REMETELHNGYR-----AFAFARYKTSKRTWYDCTLEKAYSAEK-- 61
 DB 25 REMPLNHAARRRGVGPMTWDCGLAAYAYONY-----ANORADDCGM 67
 OY 62 --SEEPSSEENVDFSAATLNIPILEAGNSWMSSEIFELRGKRYNKN---GKT-SNINAM 114
 DB 68 IHSDCPYGEN-----LAAAFPOLNAGAVAMMD--EKQWYDYSNNTCAKVCCHYQV 120
 OY 115 VMDSHDKGCAVYDC-SGKTHVCGGCP 141
 DB 121 VMKRSVRLGCAVRCSGWFITCNDP 148
 RESULT 27
 ID VA3_SOLIN STANDARD; PRT; 234 AA.
 AC P35778; 016135; 09TW22;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Venom allergen III precursor (Allergen Sol r 3) (Sol r III).
 OS Solenopsis invicta (Red imported fire ant).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Apocrita;
 OC Aculeata; Formicidae; Myrmicinae; Solenopsis.
 OX NCBI_TaxID=13686;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE-Venom;
 RA Hoffman D.R.; Farrar D.; Schmidt M.; McConnell T.J.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE OF 23-234 FROM N.A.
 RA MEDLINE=96051059; PubMed=8586864;
 RA Hoffman D.R.;
 RT "Fire ant venom allergy.";
 RL Allergy 50:535-544(1995).
 RN 13
 RP SEQUENCE OF 23-234.
 RC TISSUE-Venom;
 RA Hoffman D.R.; PubMed=8423273;
 RA Hoffman D.R.;
 RT "Allergens in Hymenoptera venom XXIV: the amino acid sequences of
 imported fire ant venom allergens Sol I II, Sol I III, and Sol I
 IV.";
 RL J. Allergy Clin. Immunol. 91:71-78(1993).
 RN 14
 RP PARTIAL SEQUENCE OF 23-45.
 RC TISSUE-Venom;
 RA MEDLINE=90285439; PubMed=2355158;
 RA Hoffman D.R.; Smith A.M.; Schmidt M.; Moffitt J.E.; Guralnick M.;
 RT "Allergens in Hymenoptera venom XXII. Comparison of venoms from two
 species of imported fire ants, *Solenopsis invicta* and *richerti*.";
 RL J. Allergy Clin. Immunol. 85:988-996(1990).
 RN 15
 RP -1- DISEASE: THE MOST COMMON CAUSE OF INSECT VENOM ALLERGY IN THE
 SOUTH-EASTERN UNITED STATES IS THE IMPORTED FIRE ANT.
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
 CC INSECTS AG/AGS; FUNGI SC7/SC14 AND PLANTS PR-1.
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 CC -----
 CC EMBL; AF012919; AAB65434.1; -
 DR PIR; B37330; B37330.
 DR PIR; C44582; C44582.
 DR HSP; P04284; ICPE.
 DR InterPro; IPR001283; Allrgn_V5/Tpx1.
 DR Pfam; PF00188; SCP; 1.
 DR PRINTS; PR00837; V5TPXLIKE.
 DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.
 DR SMART; SM00198; SCP; 1.
 DR PROSITE; PS01009; SCP_AG5_PRL_SC7_1; 1.
 DR PROSITE; PS01010; SCP_AG5_PRL_SC7_2; 1.
 KW Venom; Allergen; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 234 VENOM ALLERGEN III.
 FT DISULFID 26 41 BY SIMILARITY.
 FT DISULFID 31 125 BY SIMILARITY.
 FT DISULFID 52 118 BY SIMILARITY.
 FT DISULFID 198 216 BY SIMILARITY.
 FT COMPLECT 183 183 G -> E (IN REF. 3).
 FT COMPLECT 194 194 T -> S (IN REF. 3).
 FT COMPLECT 199 199 G -> A (IN REF. 3).
 SQ SEQUENCE 234 AA; 26351 MW; 539F510B59941D83 CRC64;
 Query Match 9.6%; Score 96; DB 1; Length 234;
 Best Local Similarity 24.0%; Pred. No. 0.13; Mismatches 73; Indels 34; Gaps 6;
 Matches 41; Conservative 23;
 OY 15 DDMREMETELHNGRAAFARNTK-----TSKRTWYDCTLEKAYSAEKSEE 64
 DB 62 DKKATVYKINNELRQVAVSGKMGNGTPOPPAKPAPNLTWPELATIAORMANOCFTF 121
 OY 65 PSSEENVDFVS-----AAT-----LNIPLEAGNSWMSSEIFELRGKRYNKNKTSNI-- 111
 DB 122 HDG-CRNERFVAGQNTATSSGKKNKSTPHEMLLWYNVADFDNRNISPSPDDNIIIM 180
 OY 112 ----ANNWMDSHDKGCAVY----DCSGTHVCGCGPEAKGDKTIVE 152
 DB 181 KVGHYTOIYMAKTKIGCGRIMKEPDNMTKHYLVACNYGAGNVLSAPIYE 231
 RESULT 28
 ID VA3_SOLRI STANDARD; PRT; 211 AA.
 AC P35779;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Venom allergen III (Allergen Sol r 3) (Sol r III).
 OS Solenopsis richteri (Black imported fire ant).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
 OC Aculeata; Formicidae; Myrmicinae; Solenopsis.
 OX NCBI_TaxID=30203;
 RN 11
 RP SEQUENCE.
 RA MEDLINE=98049167; PubMed=9389299;
 RA Hoffman D.R.;
 RT "Reactions to bees common species of fire ants.";
 RL J. Allergy Clin. Immunol. 100:679-683(1997).
 RN 12
 RP SEQUENCE OF 1-20.
 RA MEDLINE=90285439; PubMed=2355158;
 RA Hoffman D.R.; Smith A.M.; Schmidt M.; Moffitt J.E.; Guralnick M.;
 RT "Allergens in Hymenoptera venom XXII. Comparison of venoms from two
 species of imported fire ants, *Solenopsis invicta* and *richerti*.";
 RL J. Allergy Clin. Immunol. 85:988-996(1990).
 RN 13
 RP -1- DISEASE: THE MOST COMMON CAUSE OF INSECT VENOM ALLERGY IN THE

CC SOUTHEASTERN UNITED STATES IS THE IMPORTED FIRE ANT.
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
 CC INSECTS AG3/AG5; FUNGI SCT/SCI4 AND PLANTS PR-1.
 CC PIR: D60727; D60727.
 DR HSP: P04284; ICPE.
 DR InterPro: IPR001283; Allrgn_V5/TPx1.
 DR Pfam: PF00188; SCP; 1.
 DR PRINTS: PR00837; V5TPX1KE.
 DR PRODOM: PD000542; Allrgn_V5/TPx1; 1.
 DR SMART: SM00198; SCP; 1.
 DR PROSITE: PS01009; SCP_AGS_PRL_SCT_1; 1.
 DR PROSITE: PS01010; SCP_AGS_PRL_SCT_2; 1.
 DR Venom: Allergen.
 SQ SEQUENCE 211 AA; 23869 MW; 99683BA72844E9B CRC64;

Query Match
 Best Local Similarity 21.5%; Score 95.5; DB 1; Length 211;
 Matches 38; Conservative 21; Mismatches 71; Indels 47; Gaps 6;

DB 15 DDMEHTEFHNGYRAAFAANK-----TSKRTMYD-----CTLE 51
 40 DAEDDAVKNHKLKRVASGKMGKNGPQPAVAKPMLTWDPDLATIAQRMANOCTEE 99
 QY 52 EKAKSKSEKS-----EEPSSEENVDSFAATLNIPLDAGNSWSEIFELRGKYNNKG 106
 DB 100 HDACRANVERAVGONIAATSSGKNSLTSDML-----LWYNEKDFNRWISSFP 151
 QY 107 KTSNI-----ANNVMSHDKLCQAVY-----DCSGRTVVCQYGPAGKDGKTYIE 152
 DB 152 SDGNILMHVGHVQTQYVMAKTKKIGCRIMKEDNNKHYLVNCGPAGNVYLAQIYE 208

RESULT 29
 VAS_POLFU STANDARD; PRT; 205 AA.
 ID VAS_POLFU
 AC P35780;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Venom allergen 5 (Antigen 5) (AG5) (Allergen pol f 5) (pol f V).
 OS Polistes fuscatus (Paper wasp).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
 OC Aculeata; Vespoidea; Vespidae; Polistinae; Polistes.
 ON NCBI_TaxID=30207;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=94044316; PubMed=8227862;
 RA Hoffman D.R.;
 RT Allergens in Hymenoptera venom. XXV: The amino acid sequences of
 RT antigen 5 molecules and the structural basis of antigenic cross-
 RT reactivity.*;
 RL J. Allergy Clin. Immunol. 92:707-716(1993).
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
 CC INSECTS AG3/AG5; FUNGI SCT/SCI4 AND PLANTS PR-1.
 CC PIR: E44522; E44532.
 DR HSP: P04284; ICPE.
 DR InterPro: IPR001283; Allrgn_V5/TPx1.
 DR Pfam: PF00188; SCP; 1.
 DR PRINTS: PR00837; V5TPX1KE.
 DR PRODOM: PD000542; Allrgn_V5/TPx1; 1.
 DR SMART: SM00198; SCP; 1.
 DR PROSITE: PS01009; SCP_AGS_PRL_SCT_1; 1.
 DR PROSITE: PS01010; SCP_AGS_PRL_SCT_2; 1.
 DR Venom: Allergen.
 FT DISULFID 4 16 BY SIMILARITY.
 FT DISULFID 8 104 BY SIMILARITY.
 FT DISULFID 28 96 BY SIMILARITY.
 FT DISULFID 171 188 BY SIMILARITY.
 SQ SEQUENCE 205 AA; 23068 MW; 77308250FBEF357 CNC64;

Query Match
 Best Local Similarity 18.9%; Score 95; DB 1; Length 205;
 Matches 37; Conservative 30; Mismatches 79; Indels 50; Gaps 7;

DB 2 GDYSICQGRK-----DDMRKREFTLHNGYRAAFAANKYKT----- 38
 DB 11 GHIVQYQESTKRPKNADKVIKSGPTFEERKLVNENRFRQYAGQLETRNGPQ 70
 QY 39 ---SKRTVYCTLEEKAKSKAKSEEPSEENVDSFAATLNIPLDAGNS----- 89
 DB 71 PAASDNNILVMDLHIAQVMAQQQLLVHDKCRKTKYVQV-NIAVAGSKLPDVS 129
 QY 90 ---WSEIFELRGKYNNK-----GKTSNIANNVMSHDKLCQAVYDCSRT---HV 135
 DB 130 LRLWNEKVDN---YNKGITRNGKGVGHYQYVMAKTKKIGCSGLYMRNNMQHYL 186
 QY 136 VCOYGPAGKDGKTYIE 151
 DB 187 ICNYPGAGNYLGOLPY 202

RESULT 30
 YJH9_YEAST STANDARD; PRT; 299 AA.
 ID YJH9_YEAST
 AC P47032;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 30.6 kDa protein in SCP160-SMC3 intergenic region
 DE precursor.
 DE YJ079C OR J1022.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 ON NCBI_TaxID=4932;
 RN [1]
 RP SOURCE FROM N.A.
 RC STRAIN=8288C;
 RX MEDLINE=26093911; PubMed=7483841;
 RA Botes E., Schaffr-Gerstenschlaeger I., Chalwatzi N., Baur A.,
 RA Zimmermann F.K.;
 RA Zimmermann F.K.;
 RT Sequence analysis of a 33.1 kb fragment from the left arm of
 RT Saccharomyces cerevisiae chromosome X, including putative proteins
 RT with leucine zippers, a fungal Zn(II)-Cys6 binuclear cluster domain
 RT and a putative alpha 2-SCB-alpha 2 binding site.*;
 RL Yeast 11:681-689(1995).
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
 CC INSECTS AG3/AG5; FUNGI SCT/SCI4 AND PLANTS PR-1.
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 CC EMBL: 249354; CAA89372.1;
 CC EMBL: X83502; CAA58491.1;
 DR EMBL: X88851; CAA61315.1;
 DR HSP: P04284; ICPE.
 DR SGD: S0003615; YJL079C.
 DR InterPro: IPR001283; Allrgn_V5/TPx1.
 DR Pfam: PF00188; SCP; 1.
 DR PRINTS: PR00837; V5TPX1KE.
 DR PRODOM: PD000542; Allrgn_V5/TPx1; 1.
 DR SMART: SM00198; SCP; 1.
 DR PROSITE: PS01009; SCP_AGS_PRL_SCT_1; 1.
 DR PROSITE: PS01010; SCP_AGS_PRL_SCT_2; 1.
 DR Hypothetical protein; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 299 HYPOTHEITICAL PROTEIN YJL079C.

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FT DOMAIN 102 165 ALA/SER/THR-RICH.
SQ SEQUENCE 299 AA; 30634 MW; A116769CA87C5679 CRC64;

Query Match 9.5%; Score 95; DB 1; Length 299;
Best Local Similarity 22.0%; Pred. No. 0.22;
Matches 36; Conservative 27; Mismatches 43; Indels 58; Gaps 10;

QY 14 DDDREFFTEL---HNGYR-----AAFAANYKTSKARTMYDC--TLEEK 53
DB 156 DSDLSDBASVLAHKKKALAKDTPALMSDPLASIDYADN-----TDCGILTH- 208
QY 54 AKKAEKCESEPSSEENVDFSAATLNIPL-----EAGNSWSEI--FELRGKVTNKG 106
DB 209 -----SCGPYGE-----NLALGTGCPALVADAVYINISYDFSNPGEFSN- 247
QY 107 KTSNINAMWDSHDKLCAVDCSGK--THVVCQYCPKAGDK 148
DB 248 -TGFHTGVYMKSTYGVCGIKTCGANGDYTCSTYPAGNYGE 290

RESULT 31
PR1_SAMN1 STANDARD; PRT; 167 AA.
ID PR1_SAMN1
AC 041359;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pathogenesis-related protein PR-1 type precursor.
OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Dipsacales; Adoxaceae; Sambucus.
OX NCBI_Taxid:4202;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-abscission zone;
RA Coupe S.A., Taylor J.E., Roberts J.A.;
RA Submitted (DEC1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC AGAINST PATHOGENS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPO MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC
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CC
CC EMBL; 246947; CAAB7071.1;
CC HSSP; P04284; ICFE.
CC InterPro; IPR001283; Allrgn_V5/Tpx1.
CC Pfam; PF00188; SCP.1.
CC PRINTS; PR00837; VSTPLIKE.
CC ProDom; PD000542; Allrgn_V5/Tpx1.1.
CC SMART; SM00198; SCP.1.
CC PROSITE; PS01009; SCP_AGS_PRL_SCP1.1.
CC PROSITE; PS01010; SCP_AGS_PRL_SCP2.1.
CC Plant defense; Pathogenesis-related protein; Signal.
CC SIGNAL 1 25
CC CHAIN 30 167 PATHOGENESIS-RELATED PROTEIN PR-1 TYPE.
CC DISULFID 72 144 BY SIMILARITY.
CC DISULFID 117 123 BY SIMILARITY.
CC DISULFID 139 153 BY SIMILARITY.
CC SEQUENCE 167 AA; 18410 MW; 4F2B853269592E53 CRC64;
SQ

Query Match 9.5%; Score 94.5; DB 1; Length 167;
Best Local Similarity 23.2%; Pred. No. 0.12;
Matches 42; Conservative 18; Mismatches 50; Indels 71; Gaps 9;

QY 4 YSLCQREKIDDMREMTTELHNGYR-----AAFAANYKTSKARTMYDC 49

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DB 25 ILSAQ-----NSQDYVDANHAARSANVNGPYTWDSVAAPFAFQAGSR-----AGCR 73
QY 50 LEEKAKSAKSEKSEPSSEENVDFSAATLNIPLAENSMWSIEELGK-----100
DB 74 LVH-----SDPFRGE-----NLARGSG-----FELGRNADWMAE 106
QY 101 --YVNNNGT-----SNANMWDSHDKLCAVDC--SKTHVVCQYCPKAGDKTI 150
DB 107 RNDINNTWTCAKPGVCGHTGVYMKRSVRLGCAVRCNANMFICNTSPNGNTAGQRP 166
QY 151 Y 151
DB 167 Y 167

RESULT 32
CRS1_HUMAN STANDARD; PRT; 249 AA.
ID CRS1_HUMAN
AC P54107; Q13248; Q00698; Q14082;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cysteine-rich secretory protein-1 precursor (Acidic epididymal
DE glycoprotein homolog) (AEG-1-like protein) (ARP).
GN AEG1 OR CRISP-1.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A. (LONG ISOFORM), AND SEQUENCE OF 22-41.
RX MEDLINE-96270732; PubMed-8665901;
RA Kraetschmar J., Haendler B., Eberspaecher U., Roostermann D.,
RA Donner P., Schlenker W.-D.;
RA "The human cysteine-rich secretory protein (CRISP) family. Primary
RA structure and tissue distribution of CRISP-1, CRISP-2 and CRISP-3."
RA Eur. J. Biochem. 236:827-836(1996).
RN [2]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RX MEDLINE-96103955; PubMed-8543280;
RA Hayashi M.;
RA "Analysis of the human acidic epididymal glycoprotein-like molecule:
RA isolation of cDNA and tissue localization."
RA Hokkaido Igaku Zasshi 70:743-753(1995).
RN [3]
RP SEQUENCE FROM N.A. (LONG ISOFORM), AND CHARACTERIZATION.
RX MEDLINE-96435914; PubMed-8838800;
RA Hayashi M., Fujimoto S., Takano H., Uehiki T., Abe K., Ishikura H.,
RA Hayashi M.C., Kirchhoff C., Ishibashi T., Kasahara M.;
RA "Characterization of a human glycoprotein with a potential role in
RA sperm-egg fusion: cDNA cloning, immunohistochemical localization,
RA and chromosomal assignment of the gene (AEG1).";
RA Genomics 32:367-374(1996).
RN [4]
RP SUBCELLULAR LOCATION: LOCATED IN THE LUMEN AND EPITHELIUM OF
RP DISTAL DUCTUS EPIDIDYMUS AND EPIDIDYMAL DUCTS, AND ON THE
RP POSTACROSOMAL REGION OF THE SPERM HEAD.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a
CC short form/CRISP-1 delta; may be produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: CAPUT CORPUS AND CAUDA REGIONS OF THE
CC EPIDIDYMUS, THE DUCTUS DEFERENS, SPERM AND SEMINAL PLASMA.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPO MAMMALIAN SC7/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC
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DR EMBL: X95237.1: CA64523.1: -
 DR EMBL: X95237.1: CA64523.1: -
 DR EMBL: S80310.1: AB83889.1: -
 DR EMBL: D38451.1: BA07483.1: -
 DR GenBank: HGNC:304: ABGL.
 DR MIM: 601193: -
 DR InterPro: IPR001283: Allrgn_V5/Tpx1.
 DR Pfam: PF00188: SCP.1.
 DR PRINTS: PR00837: V5TPXLKE.
 DR ProDom: PD000542: Allrgn_V5/Tpx1.1.
 DR SMART: SM00198: SCP.1.
 DR PROSITE: PS01009: SCP_AGS_PRI_SCP_1: 1.
 DR PROSITE: PS01010: SCP_AGS_PRI_SCP_2: 1.
 DR GlycoProtein: Signal; Multigene family; Alternative splicing.
 FT SIGNAL 1 21
 FT CHAIN 22 249 Cysteine-rich secretory protein-1.
 FT CARBOHD 230 230 N-LINKED (GLCNAC...)
 FT VARSPLIC 178 178 E->D (IN SHORT ISOFORM).
 FT VARSPLIC 179 249 MISSING (IN SHORT ISOFORM).
 FT CONFLICT 22 22 K->E (IN REF. 2 AND 3).
 FT CONFLICT 97 97 T->A (IN REF. 2 AND 3).
 SO SEQUENCE 249 AA; 28481 MW; 85BED3DEAD62A9C CRC64;
 Query Match 9.5%; Score 94.5; DB 1; Length 249;
 Best Local Similarity 23.7%; Pred. No. 0.19; Indels 75; Gaps 14;
 Matches 51; Conservative 22; Mismatches 67; Indels 75; Gaps 14;
 QY 9 GREKDDDM---REMFELHNGYRAAFARNTKSKRMVYDCTLEKAYKSAKSEEP 65
 DB 29 QFNKLVTDLPNVEELIVNHNALRRVVP--PASNNLTKSM-----SEEA 71
 QY 66 SSEEENVDVFA---ATINIPLE-----AGNSW-----SEIFELGKVVY--- 103
 DB 72 A---QNAKIFSKYCMETESNPLERRLPNFCGNNHMTSYVMSVIT---GVWYSEST 125
 QY 104 -KNGK-----TSNANWVMSHDKLGCAVYCC---SGKHVVCY---GPEAK 144
 DB 126 FKNGEWTDDDDITTDHYTQVWATSTYLISGALASCRGGSPRLVYCHCHGNDPEK 185
 QY 145 GDGKTYIEGAPCSGSDYAGVYCDODDQNLICI 179
 DB 186 NEP---YKTVGVCACPS-----NCEBKICITNPCI 212
 RESULT 33
 ID SC7_SCHCO STANDARD; PRT; 204 AA.
 AC P35794.
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Fruiting body protein SC7 precursor.
 GN SC7
 OS Schizophyllum commune (Bracket fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Schizophyllales; Schizophyllum.
 OX NCBI_TaxID=5334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94065639; PubMed=8245835;
 RA Schuren F.H.J.; Asgelrsdottrir S.A.; Kothe E.M.; Scheer J.M.J.;
 RA Wessels J.G.H.;
 RT "The Sc7/Sc14 gene family of schizophyllum commune codes for
 RT extracellular proteins specifically expressed during fruit-body
 RT formation.";
 RL J. Gen. Microbiol. 139:2083-2090(1993).
 CC -1- SUBCELLULAR LOCATION: secreted.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED ONLY IN FRUITING DIKARYONS.
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
 CC INSECTS AGS/AGS; FUNGI SC7/SC14 AND PLANTS PR-1.
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL: M81722.1: AAA16207.1: -
 DR PIR: S27448; S27448.
 DR HSP: P04284; ICEE.
 DR InterPro: IPR001283: Allrgn_V5/Tpx1.
 DR Pfam: PF00188: SCP.1.
 DR PRINTS: PR00837: V5TPXLKE.
 DR ProDom: PD000542: Allrgn_V5/Tpx1.1.
 DR SMART: SM00198: SCP.1.
 DR PROSITE: PS01009: SCP_AGS_PRI_SCP_1: 1.
 DR PROSITE: PS01010: SCP_AGS_PRI_SCP_2: 1.
 DR Fruiting body; Signal; Multigene family.
 FT SIGNAL 1 16
 FT CHAIN 17 204 FRUITING BODY PROTEIN SC7.
 FT CARBOHD 80 80 N-LINKED (GLCNAC...)
 FT CARBOHD 118 118 N-LINKED (GLCNAC...)
 FT CARBOHD 134 134 N-LINKED (GLCNAC...)
 SO SEQUENCE 204 AA; 22302 MW; 47FIC845ADFA2FC9 CRC64;
 Query Match 9.4%; Score 94; DB 1; Length 204;
 Best Local Similarity 21.6%; Pred. No. 0.17; Indels 42; Gaps 5;
 Matches 35; Conservative 23; Mismatches 62; Indels 42; Gaps 5;
 QY 10 REKDDDMR-----EMFELHNGYRAAFARNTKSKRMVYDCTLEK 53
 DB 34 RSPIDIDRSADALANAPPOSEIDQKLNHNRONG-----AVALWMDLSDK 86
 QY 54 AKSAKSEEPSESEENVDVFAATINIPLE-----EAGNSWSEIFELKRYNNKGTSN 110
 DB 87 ADPAKSCITWHSNCGNLAWFSPQAKFKMTISGIGVGNNALEPNTYNTTISGAGHWQ 146
 QY 111 IANWVMSHDKLGCAVYDCSKT-----HYVCY 139
 DB 147 V---VWKSITSVGCAVSCPGLGKRPDPKTLMTVYCNV 185
 RESULT 34
 ID AGS_RAT STANDARD; PRT; 246 AA.
 AC P12020.
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sperm-coating glycoprotein precursor (SCP) (acidic epididymal
 DE glycoprotein) (Protein D) (Protein E) (Staloprotein)
 DE (32 kDa epididymal protein).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Epididymis;
 RA BROOKS D.E.; Means A.R.; Wright E.J.; Singh S.P.; Tiver K.K.;
 RA MEDLINE=87053995; PubMed=3780731;
 RT "Molecular cloning of the cDNA for androgen-dependent sperm-coating
 RT glycoproteins secreted by the rat epididymis.";
 RL Eur. J. Biochem. 161:13-18(1986).
 CC -1- FUNCTION: THIS PROTEIN IS SUPPOSED TO HELP SPERMATOZOA UNDERGO
 CC FUNCTIONAL MATURATION WHILE THEY MOVE FROM THE TESTIS TO THE

```

CC DOCTUS DEFENS.
CC -1- INDUCTION: BY ANDROGENS.
CC MISCELLANEOUS: SCP IS AN ANDROGEN-DEPENDENT PROTEIN, WHICH IS
CC SECRETED BY THE EPIDIDYMAL EPITHELIUM AND THEN BECOMES DIFFERED
CC WITH THE SPERM SURFACE. TWO MAJOR VARIANT PROTEIN D AND E DERIVED
CC FROM EACH OTHER BY THEIR CARBOHYDRATE SIDE CHAINS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X04643; CAA28304.1;
CC PIR: M31173; AAB59716.1;
CC PIR: A40918; A40918.
CC InterPro: IPR001283; Allrgn_V5/Tpx1.
CC Pfam: PF00188; SCP.1.
CC PRINTS: PR00837; V5TPXLIKE.
CC PRODOM: PD000542; Allrgn_V5/Tpx1.1.
CC SMART: SM00198; SCP.1.
CC PROSITE: PS01009; SCP_AG5_PRL_SC7_1; 1.
CC PROSITE: PS01010; SCP_AG5_PRL_SC7_2; 1.
CC KW: Sperm; Glycoprotein; Signal.
CC FT: SIGNAL 1 19
CC FT: CHAIN 1 19
CC FT: MOD_RES 20 20
CC FT: CARBOHYD 32 32
CC FT: CARBOHYD 85 85
CC FT: CARBOHYD 147 147
CC FT: CARBOHYD 213 213
CC SEQUENCE 246 AA; 27847 MW; 585207C7CF7CE9D CRC64;

Query Match 9.48; Score 94; DB 1; Length 246;
Best Local Similarity 23.28; Pred. No. 0.21; Mismatches 82; Indels 44; Gaps 9;
Matches 45; Conservative 23;

OY 17 MRKMTLEHNGYRAFRNRTKTKMTMYDCTLEKAYSAKCEPSESEENV--- 72
DB 40 VDEEILINKHNDLRNTPSP--GSDLLRVEBMDADAVNNAKNCIYNHSPHQHTTTLK 97
OY 73 ---DVFSATINIPLEAGN---SWNSEIFE-LRGKYVKNKG-KTSNIANNVDSHDKLG 124
DB 98 CGENLEFMA--NYPASMSVYIDWDYDSELDFFVGFGRKGVGVGHYQVYVNSTFLVAC 154
OY 125 AVVDCSG--KTHVVCQYGFPEAKGDK--TIYEGAPC----- 157
DB 155 GVAECDDPPLKFFYVCHYCPGNTVGRILSPYTEGEPCDSCPGNCBDGLCTNSCEYEDNY 214
OY 158 SRCSDYGAGVTCD 171
DB 215 SNGCDLKKVSCDD 228

RESULT 35
PRL3_HORVU STANDARD: PRT: 164 AA.
AC P35792;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE Pathogenesis-related protein PRB1-2 precursor.
OS Hordeum vulgare (Barley)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-CV. PAKNON RESISTANT; TISSUE-Leaf;
RX MEDLINE=95036024; PubMed=7524728;
RA Mouradov A., Mouradova E., Scott K.J.;
RT "Gene family encoding basic pathogenesis-related 1 proteins in
barley."
RL Plant Mol. Biol. 26:503-507(1994).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC AGAINST PATHOGENS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Z26320; CAA81229.1;
CC PIR: S37188; S37188.
CC HSP: P04284; ICEF.
CC InterPro: IPR001283; Allrgn_V5/Tpx1.
CC Pfam: PF00188; SCP.1.
CC PRINTS: PR00837; V5TPXLIKE.
CC PRODOM: PD000542; Allrgn_V5/Tpx1.1.
CC SMART: SM00198; SCP.1.
CC PROSITE: PS01009; SCP_AG5_PRL_SC7_1; 1.
CC PROSITE: PS01010; SCP_AG5_PRL_SC7_2; 1.
CC KW: Plant defense; Pathogenesis-related protein; Signal; Multigene family.
CC FT: SIGNAL 2 144
CC FT: CHAIN 2 144
CC FT: MOD_RES 25 25
CC FT: MOD_RES 25 25
CC FT: DISULFID 68 140
CC FT: DISULFID 113 119
CC FT: DISULFID 135 139
CC SEQUENCE 164 AA; 17679 MW; DB8722DB/4EEB390 CRC64;

Query Match 9.38; Score 92.5; DB 1; Length 164;
Best Local Similarity 24.08; Pred. No. 0.18; Mismatches 56; Indels 43; Gaps 6;
Matches 36; Conservative 15;

OY 25 HNGYRA-----AFARNYTSKMTMYDCTLEKAYSAKCEPSESEE 70
DB 35 HNAARSVGVGAVSWSTKLQAFQNTANOR---INDKLOHSG-----GPGE 79
OY 71 NVDFSATINIPLEAGNSWNSSEIFEELRGKYVKNKGK-----SNIANVYVDSHDKLG 123
DB 80 NIFGSGADMKAAADVNSWNE-----KRDYNGSNTCAAGKYCGHYQVYVNSTFLVAC 154
OY 124 CAVVDCSGK--KTHVVCQYGFPEAKGDKTIY 151
DB 135 CARVVCNNRGVETTCNTEPRGNTYQGRPY 164

RESULT 36
PRL3_HORVU STANDARD: PRT: 164 AA.
AC P35793;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE Pathogenesis-related protein PRB1-3 precursor (PR-1B) (HV-8).
OS Hordeum vulgare (Barley)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. PAKNON resistant, and cv. NK1558; TISSUE-Leaf;

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RA MEDLINE-95036024; PubMed-7524728;
RA Mouradov A., Mouradova E., Scott K.J.;
RT Gene family encoding basic pathogenesis-related 1 proteins in
RT barley.
RL Plant Mol. Biol. 26:503-507(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. Pallas; TISSUE-Leaf;
RC MEDLINE-94281675; PubMed-8012045;
RA Bryngelsson T., Sommer-Knudsen J., Gregersen P.L., Collinge D.B.,
RA Ek B., Thordal-Christensen H.;
RT "Purification, characterization, and molecular cloning of basic PR-1-
RT type pathogenesis-related proteins from barley."
RL Mol. Plant Microbe Interact. 7:267-275(1994)
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEEPEN REACTION OF PLANTS
CC AGAINST PATHOGENS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib.ch).
CC -----
DR EMBL; Z26321; CAA81230.1;
DR EMBL; Z26333; CAA81234.1;
DR EMBL; X74940; CAA52894.1;
DR PIR; S37189; S37189.
DR PIR; S37209; S37209.
DR PIR; S37167; S37167.
DR HSP; P04284; ICFE.
DR InterPro; IPR001283; Allrgn_V5/TPX1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPX1KE.
DR ProDom; PD000542; Allrgn_V5/TPX1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; SCP_AG5_PRL_SCP_1; 1.
DR PROSITE; PS01010; SCP_AG5_PRL_SCP_2; 1.
KW Plant defense; Pathogenesis-related protein; signal; Multigene family.
FT SIGNAL 1 24
FT CHAIN 25 164 PATHOGENESIS-RELATED PROTEIN PR1-3.
FT MOD_RES 25 25 PYROLIDONE CARBOXYLIC ACID
FT DISULFID 68 140 (BY SIMILARITY).
FT DISULFID 113 119 BY SIMILARITY.
FT DISULFID 135 150 BY SIMILARITY.
SQ SEQUENCE 164 AA; 17697 MW; DA4B279B9F5C50C6 CRC64;

Query Match 9.3%; Score 92.5; DB 1; Length 164;
Best Local Similarity 24.7%; Pred. No. 0.18;
Matches 37; Conservative 14; Mismatches 56; Indels 43; Gaps 6;

OY 25 HNGYRA-----AFARITKTSKMTNRYDCTLEKAYKSAEKSEPSSEEE 70
DB 35 HNAARAAVGVAVSNSTLQAFANQANOR-----INDKIQHSG-----GPYGE 79
OY 71 NDVFSAAATLNIPLDAGNSWMSSEIFELRGKRYNNKNGKT-----SNIANMWDSHDKLG 123
DB 80 NIFWGSAGADWKAASDAVSWVSE-----KKDDYSNTCAAGKVCYGHYQVWRASTSIG 134
OY 124 CAVVDCSGK--THVVCQYGEPAKDGKTIY 151
DB 135 CARVVCNNRGVFTICNTEPRGNIVGQKPY 164

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DT 15-JUL-1999 (Rel. 38, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE Venom allergen 5 (antigen 5) (AG5) (Allergen Vesp m 5).
OS Vespa manducaria (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidae; Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=446;
RN [1]
RP SEQUENCE.
RC TISSUE-Venom;
RC Hoffman D.R., Schmidt J.O.;
RL Submitted (FEB-1998) to the SWISS-PROT data bank.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
CC InterPro; IPR001283; Allrgn_V5/TPX1.
CC Pfam; PF00188; SCP; 1.
CC PRINTS; PR00837; V5TPX1KE.
CC ProDom; PD000542; Allrgn_V5/TPX1; 1.
CC SMART; SM00198; SCP; 1.
CC PROSITE; PS01009; SCP_AG5_PRL_SCP_1; 1.
CC PROSITE; PS01010; SCP_AG5_PRL_SCP_2; 1.
KW Venom; Allergen.
FT DISULFID 4 16 BY SIMILARITY.
FT DISULFID 8 101 BY SIMILARITY.
FT DISULFID 26 94 BY SIMILARITY.
FT DISULFID 168 185 BY SIMILARITY.
SQ SEQUENCE 202 AA; 22547 MW; 68635157B014EF CRC64;

Query Match 9.3%; Score 92.5; DB 1; Length 202;
Best Local Similarity 23.4%; Pred. No. 0.23;
Matches 39; Conservative 27; Mismatches 70; Indels 31; Gaps 7;

OY 11 ERIDDDMMETELHNGYRAAPARNTK-----SKRTMYDCTLEKAYKSAEK 60
DB 40 EKLE-----ILQGHNEKOKANGLETNGKGGPOPPAKSANTLVNDELQIAQVWAGQ 93
OY 61 C-----SEPSSEEN--DVESATLNIPLDAGNSWMSSEIFELR-GKRYNNKNGTS 109
DB 94 CDYGHDCRNRAKTSVGNQNAENGSTAFSEASVSNNVQMADEVKNYQYGSYKNNLEIVG 153
OY 110 NIANWYDSHDKCAVADC--SG--KTHVVCQYGEPAKDGKTIY 152
DB 154 HTYQWMAKTEICGSGIKYIENGWHRHLYCNGYFAGNIGNEPIYE 200

RESULT 38
PRLA_TOBAC STANDARD; PRT; 168 AA.
AC P08299;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pathogenesis-related protein 1A precursor (PR-1a).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eusterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. Samsun NN;
RC MEDLINE-86015528; PubMed-3658669;
RA Cornelissen B.J.C., Horowitz J., van Kan J.A.L., Goldberg R.B.,
RA Bol J.F.;
RT "Structure of tobacco genes encoding pathogenesis-related proteins
RT from the PR-1 group."
RL Nucleic Acids Res. 15:6799-6811(1987).

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RESULT 37
VAS_VESMA STANDARD; PRT; 202 AA.
AC P81657;
DT 15-JUL-1999 (Rel. 38, Created)

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SQ SEQUENCE 164 AA: 17683 MW: 80972FF654F77395 CRC64;
Query Match 9.0%; Score 89.5; DB 1; Length 164;
Best Local Similarity 24.0%; Pred. No. 0.33;
Matches 36; Conservative 15; Mismatches 56; Indels 43; Gaps 6;

OY 25 HNGYRA-----AARNYKSKRMVYDCTLEKAYKSAKCESEPSSEEE 70
   |||
DB 35 HNAARSVGVGVAVSSTKLOAFQNTANOR-----INDCMLDHS-----GPYCE 79
OY 71 NNDVFSATINIPLEAGNSWSEIFELRGVYKNGKT-----SNIANVWDSHDKLG 123
DB 80 NIFGSGADWKRASDVMSWSE-----KNDIYGSNTCAAGVKGHYGVVRASTSIG 134
OY 124 CAYVDSGK--THVYCGYGPPEAKGDKRTY 151
DB 135 CARVVCNNRNGVITCNTEPRGNITIGKPY 164

RESULT 40
VAS_POLEX STANDARD; PRT; 205 AA.
AC P35759;
AD 01-JUN-1994 (Rel. 29, Created)
AD 01-JUN-1994 (Rel. 29, Last sequence update)
AD 15-JUL-1998 (Rel. 36, Last annotation update)
DE Venom allergen 5 (Antigen 5) (AG5) (Allergen Pol e 5) (Pol e V).
OS Polistes exclamans (Paper wasp).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidea; Vespidae; Polistinae; Polistes.
ON NCBI_Taxid=27506;
RN [1]
RP TISSUE-Venom.
RC MEDLINE=93203603; PubMed=8454859;
RX Lu G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;
RT "Sequence analysis and antigenic cross-reactivity of a venom
allergen, antigen 5, from hornets, wasps, and yellow jackets."
RL J. Immunol. 150:2823-2830(1993).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG5/AG5; FUNGI SCT/SC14 AND PLANTS PR-1.
DR HSP; P04284; ICFE.
DR PIR; A57329; A57329.
DR DR HSP; P04284; ICFE.
DR InterPro: IPR001283; Allrgn_V5/TPX1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPX1LKE.
DR PRODOM; PD000542; Allrgn_V5/TPX1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; SCP_AGS_PRL_SCT_1; 1.
DR PROSITE; PS01010; SCP_AGS_PRL_SCT_2; 1.
KW Venom; Allergen.
FT DISULFID 4 16 BY SIMILARITY.
FT DISULFID 8 104 BY SIMILARITY.
FT DISULFID 28 96 BY SIMILARITY.
FT DISULFID 171 188 BY SIMILARITY.
SQ SEQUENCE 205 AA: 22944 MW: DBE93D07316773B3 CRC64;

Query Match 8.6%; Score 86; DB 1; Length 205;
Best Local Similarity 19.2%; Pred. No. 0.88;
Matches 38; Conservative 30; Mismatches 76; Indels 54; Gaps 8;

OY 2 GYSILCOQREK-----DDDMREMTFLHNGYRAAFARNYKT----- 38
   |||
DB 11 GIHTVQYQESTKPSKNCAGVIKSVGPTBEKKLYSEHNRFRQVAGQLETRGNPQ 70
OY 39 ----SKRTMYVDTLEKAYKSAKCESEPSSEEBENVDFSAATINIPLEAGNS----- 89
DB 71 PAASDMNDLVWDELHAIQVWASOCFLVHDKCRNTAKYVQO--NIYVAGSGSLPDVVS 129
OY 90 ----WSEIFELRGVYKNN-----GKTSNIANNVWDSHDKLGA--VVDGSGKTH 134
DB 130 LITLMENEV-----KDFNYNTGITKONFAKIGHYQVWVGKTRKIGCGSLKYIENKQNH 184
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OY 135 -VYCYGPEAKGDKRTY 151
DB 185 YLTCNIGPAGNTLDOLPY 202

RESULT 41
VAS_POLAN STANDARD; PRT; 209 AA.
AC 005109;
AD 01-FEB-1994 (Rel. 28, Created)
AD 01-FEB-1994 (Rel. 28, Last sequence update)
AD 01-NOV-1997 (Rel. 35, Last annotation update)
DE Venom allergen 5 precursor (Antigen 5) (AG5) (Allergen Pol a 5) (Pol a
V) (Fragment).
OS Polistes annularis (Paper wasp).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidea; Vespidae; Polistinae; Polistes.
ON NCBI_Taxid=27505;
RN [1]
RP TISSUE-Venom.
RC MEDLINE=93203603; PubMed=8454859;
RX Lu G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;
RT "Sequence analysis and antigenic cross-reactivity of a venom
allergen, antigen 5, from hornets, wasps, and yellow jackets."
RL J. Immunol. 150:2823-2830(1993).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SCT/SC14 AND PLANTS PR-1.
DR EMBL; M98857; AAA29793.1; -.
DR HSP; P04284; ICFE.
DR InterPro: IPR001283; Allrgn_V5/TPX1.
DR Pfam: PF00188; SCP; 1.
DR PRODOM; PD000542; Allrgn_V5/TPX1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; SCP_AGS_PRL_SCT_1; 1.
DR PROSITE; PS01010; SCP_AGS_PRL_SCT_2; 1.
KW Venom; Allergen; signal.
FT NON_TER 1 4
FT SIGNAL <1 4 BY SIMILARITY.
FT CHAIN 5 209 VENOM ALLERGEN 5.
FT DISULFID 8 20 BY SIMILARITY.
FT DISULFID 12 108 BY SIMILARITY.
FT DISULFID 32 100 BY SIMILARITY.
FT DISULFID 175 192 BY SIMILARITY.
SQ SEQUENCE 209 AA: 23293 MW: 39BD9A2B51BF555B CRC64;

Query Match 8.6%; Score 86; DB 1; Length 209;
Best Local Similarity 19.2%; Pred. No. 0.9;
Matches 38; Conservative 32; Mismatches 74; Indels 54; Gaps 8;

OY 2 GYSILCOQREK-----DDDMREMTFLHNGYRAAFARNYKT----- 38
   |||
DB 15 GIHTVQYQESTKPSKNCAGVIKSVGPTBEKKLYSEHNRFRQVAGQLETRGNPQ 74
OY 39 ----SKRTMYVDTLEKAYKSAKCESEPSSEEBENVDFSAATINIPLEAGNS----- 89
DB 75 PAASDMNDLVWDELHAIQVWASOCFLVHDKCRNTAKYVQO--NIYVAGSGSLPDVVS 133
OY 90 ----WSEIFELRGVYKNN-----GKTSNIANNVWDSHDKLGA--VVDGSGKTH 134
DB 134 LITLMENEV-----KDFNYNTGITKONFAKIGHYQVWVGKTRKIGCGSLKYIENKQNH 188
```

OY 135 -VVCQYGPAAKDGKTY 151
DB 189 YILCNVGNVGLQPLP 206

RESULT 42
ITB5_HUMAN STANDARD: PRT; 799 AA.
AC P18084;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Integrin beta-5 precursor.
GN ITGB5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymic epithelium;
RX MEDLINE=90228356; PubMed=2328726;
RA Ramaswamy H., Hemler M.E.;
RT "Cloning, primary structure and properties of a novel human Integrin
beta subunit.";
RT beta subunit.";
RT EMBL J. 911561-1568(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=90319111; PubMed=23271275;
RX Suzuki S., Huang Z.S., Tanikawa H.;
RT Cloning of an Integrin beta subunit exhibiting high homology with
Integrin beta 3 subunit.";
RT Proc. Natl. Acad. Sci. U.S.A. 87:5354-5358(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=91009141; PubMed=2211615;
RX McLean J.R., Vestal D.J., Chersesh D.A., Bodary S.C.;
RT "CDNA sequence of the human Integrin beta 5 subunit.";
RT J. Biol. Chem. 265:17126-17131(1990).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strassberg R.;
RT Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
RT IT FUNCTION: INTEGRIN ALPHA-V/BETA-5 IS A RECEPTOR FOR FIBRONECTIN.
RT IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGAND.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-5
CC ASSOCIATES WITH ALPHA-V.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
CC -1- SIMILARITY: CONTAINS 1 VMPA-LIKE DOMAIN.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X53002; CAA37188.1;
DR EMBL: M35011; AAA52707.1;
DR EMBL: J05633; AAA59183.1;
DR EMBL: BC006541; AAH06541.1;
DR PIR: A35775; A35775.
DR PIR: S12534; S12534.
DR PIR: A38308; A38308.
DR PIR: S11708; S11708.
DR HSSP: P05106; 1JY2.
DR Genew: H0NC:6160; ITGB5.
DR MIM: 147561;
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002369; Integrin_B.

DR InterPro: IPR001169; Integrin_beta_C.
DR InterPro: IPR003659; Plexin-like
DR InterPro: IPR002035; VWF_A.
DR Pfam: PF00162; Integrin_B_1.
DR Pfam: PF01186; INTEGRIN.
DR PROSITE: PS00181; Integrin_B_1.
DR SMART: SM00181; EGF_1.
DR SMART: SM00001; EGF-like_1.
DR SMART: SM00187; INE_1.
DR SMART: SM00423; PSI_1.
DR SMART: SM00327; VMA_1.
DR PROSITE: PS00243; INTEGRIN_BETA_2.
DR PROSITE: PS00022; EGF_1; UNKNOWN_2.
DR PROSITE: PS01186; EGF_2; UNKNOWN_2.
KW Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
KW Repeat; Signal.
FT SIGNAL 1 23
FT CHAIN 1 799
FT TRANSMEM 24 719
FT DOMAIN 720 742
FT DOMAIN 743 799
FT DOMAIN 136 378
FT DOMAIN 465 630
FT REPEAT 465 512
FT REPEAT 513 554
FT REPEAT 555 593
FT REPEAT 594 630
FT DISULFID 28 463
FT DISULFID 36 46
FT DISULFID 39 75
FT DISULFID 49 211
FT DISULFID 202 300
FT DISULFID 259 300
FT DISULFID 401 413
FT DISULFID 433 682
FT DISULFID 461 465
FT DISULFID 476 487
FT DISULFID 484 522
FT DISULFID 489 498
FT DISULFID 500 533
FT DISULFID 528 535
FT DISULFID 530 548
FT DISULFID 535 548
FT DISULFID 550 571
FT DISULFID 569 571
FT DISULFID 571 585
FT DISULFID 576 594
FT DISULFID 587 613
FT DISULFID 606 657
FT DISULFID 610 625
FT DISULFID 619 631
FT DISULFID 625 644
FT DISULFID 635 644
FT DISULFID 641 714
FT DISULFID 651 690
FT CARBOHYD 347 347
FT CARBOHYD 460 460
FT CARBOHYD 477 477
FT CARBOHYD 505 505
FT CARBOHYD 552 552
FT CARBOHYD 586 586
FT CARBOHYD 654 654
FT CARBOHYD 705 705
FT CARBOHYD 193 193
FT CONFLICT 645 645
FT CONFLICT 792 792
SQ SEQUENCE 799 AA; 88053 MW; DTE4727CA310512B CRC64;

Query Match 8.6%; Score 86; DB 1; Length 799;
Best Local Similarity 22.0%; Pred. No. 4.6;
Matches 51; Conservative 31; Mismatches 66; Indels 84; Gaps 15;

11 EXLDDREKREFTELHNGYAAAFARVYTKMKRTMYVD-----CTLEE-KAYKSAE 59


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[4]
RN SUBCELLULAR LOCATION.
RP MEDLINE-91224081; PubMed-2026137;
RA Dixon D.C., Cutt J.R., Kleesig D.F.;
RT "Differential targeting of the tobacco PR-1 pathogenesis-related
RT proteins to the extracellular space and vacuoles of crystal
RT idioblasts."
RL EMBL J. 10:1317-1324(1991).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC AGAINST PATHOGENS.
CC SUBCELLULAR LOCATION: ACCUMULATE IN WITHIN THE VACUOLES OF
CC SPECIALIZED CELLS KNOWN AS CRYSTAL IDIOBLASTS.
CC -1- INDUCTION: SYNTHESIZED DURING PATHOGEN INFECTION OR OTHER STRESS-
CC RELATED RESPONSES.
CC -1- PPM: THREE DISULFIDE BONDS ARE PRESENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC
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CC
CC EMBL: X17681; CA33666.1; -
CC EMBL: X03454; CA329023.1; -
CC EMBL: X12487; CA31010.1; -
CC PIR: S07580; S07580.
CC HSSP: P04284; ICFE.
CC InterPro: IPR001283; Allrgn_V5/TPx1.
CC Pfam: PF00188; SCP.1.
CC PRINTS: PR00837; V5TPX1.LIKE.
CC ProDom: PD000542; Allrgn_V5/TPx1.1.
CC SMART: SM00198; SCP.1.
CC PROSITE: PS01009; SCP_AGS_PRI_SCP_1; 1.
CC PROSITE: PS01010; SCP_AGS_PRI_SCP_2; 1.
CC Plant defense; Pathogenesis-related protein; Multigene family; Signal.
CC FT SIGNAL 30
CC CHAIN 1
CC SEQUENCE 168 AA; 18583 MW; 2F2F68317C103809 CRC64;

Query Match 8.5%; Score 85; DB 1; Length 168;
Best Local Similarity 21.7%; Pred. No. 0.85;
Matches 38; Conservative 22; Mismatches 51; Indels 64; Gaps 9;

OY 7 COOREKLDMDREMFTEHNGYR-----AARARYKSKKRTMYDCTL-- 50
DB 28 CHAQSQD-----YDAHTARADYGVPLTWDDYRAIAQNTYASQ----LAADCLVH 78
OY 51 -----EKAKYSAEKSESEPSSEENDVFSATLPIPLAENGSMWSIFELGKYNK 104
DB 79 SHGQYGEHLWAGSG-----DEFLAA-----KAVEMVYNE-----KQYIAH 113
OY 105 NGKT-----SRIANWYDSDHDKAGAVDCSGKTHV/-COYGPAAKGDGKTYI 151
DB 114 DSNFCAQGVCGHYTVVWNSRVGCAVCCNGGTVISCNTPDNGVIGKSP 168

RESULT 45
PRIB_TOBAC STANDARD; PRT; 168 AA.
AC P07053;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pathogenesis-related protein 1B precursor (PR-1B).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Asteridae; eunasterids I; Solanales; Solanaceae; Nicotiana.
NCBI_TaxID=4097;

```

```

[1]
RN SEQUENCE FROM N.A.
RP STRAIN-cv. Samsun NN; TISSUE-leaf;
RA MEDLINE-90174914; PubMed-2308824;
RA Oshimi M., Harada N., Matsuka M., Oshimi Y.;
RT "The nucleotide sequence of pathogenesis-related (PR) 1b protein gene
RT of tobacco."
RL Nucleic Acids Res. 18:181-181(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-cv. Samsun NN;
RA Cornelissen B.J.C., Hooft van Hujsdijnen R.A.M., van Loon L.C.;
RA Bol J.F.;
RT Molecular characterization of messenger RNAs for 'pathogenesis-
RT related proteins 1a, 1b and 1c, induced by TMV infection of
RT tobacco."
RL EMBL J. 5:37-40(1986).
RN [3]
RP SEQUENCE OF 16-168 FROM N.A.
RA STRAIN-cv. Xanthi;
RA MEDLINE-89041576; PubMed-3186451;
RA Cutt J.R., Dixon D.D., Carr J.P., Kleesig D.F.;
RT "Isolation and nucleotide sequence of cDNA clones for the
RT pathogenesis-related proteins Pr1a, Pr1b and Pr1c of Nicotiana
RT tabacum cv. Xanthi nc induced by TMV infection."
RT Nucleic Acids Res. 16:9861-9861(1988).
RN [4]
RN SUBCELLULAR LOCATION.
RP MEDLINE-91224081; PubMed-2026137;
RA Dixon D.C., Cutt J.R., Kleesig D.F.;
RT "Differential targeting of the tobacco PR-1 pathogenesis-related
RT proteins to the extracellular space and vacuoles of crystal
RT idioblasts."
RL EMBL J. 10:1317-1324(1991).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC AGAINST PATHOGENS.
CC SUBCELLULAR LOCATION: ACCUMULATE IN WITHIN THE VACUOLES OF
CC SPECIALIZED CELLS KNOWN AS CRYSTAL IDIOBLASTS.
CC -1- INDUCTION: SYNTHESIZED DURING PATHOGEN INFECTION OR OTHER STRESS-
CC RELATED RESPONSES.
CC -1- PPM: THREE DISULFIDE BONDS ARE PRESENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC
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CC
CC EMBL: D90197; BA11221.1; -
CC EMBL: X03463; CA27183.1; -
CC EMBL: X12486; CA31009.1; -
CC EMBL: X17680; CA33665.1; -
CC PIR: B24620; B24620.
CC PIR: S07579; S07579.
CC HSSP: P04284; ICFE.
CC InterPro: IPR001283; Allrgn_V5/TPx1.
CC Pfam: PF00188; SCP.1.
CC PRINTS: PR00837; V5TPX1.LIKE.
CC ProDom: PD000542; Allrgn_V5/TPx1.1.
CC SMART: SM00198; SCP.1.
CC PROSITE: PS01009; SCP_AGS_PRI_SCP_1; 1.
CC PROSITE: PS01010; SCP_AGS_PRI_SCP_2; 1.
CC Plant defense; Pathogenesis-related protein; Multigene family; Signal.
CC FT SIGNAL 30
CC CHAIN 1
CC SEQUENCE 168 AA; 18499 MW; 61FCE3B87AF31F1 CRC64;

Query Match 8.5%; Score 84.5; DB 1; Length 168;

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Best Local Similarity 22.2%; Pred. No. 0.95; Matches 34; Conservative 23; Mismatches 53; Indels 43; Gaps 7;

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QY      21 FTLEHNGYR-----AAFAANYKTSKMRMTNYDCTLEEKAYKSAEKSEPS 66
      : : | | |
      37 YLDAHNTARADYGVBEPLTWNGVAAYQNY---VSQLAADCNLVSHGQYGENLAQSG 92
QY      67 SEENVDVFEAATLNIPLEAGNSWSEIFELRGKYNNKNGKT-----SNIANMYWDSH 119
      : : | | |
      Db  93 -----DEMTAA-----KAYEMMYDE-----KQYDHDNSTCAAGGYCGHYTYVWRNS 135
QY      120 DKLGCAVVDGSGKTHYV-CQYGEAKGDGKTIY 151
      : : | | |
      Db  136 VRGCAVRCNKNNGYVSCNTPGNYIGQSPY 168
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Search completed: July 15, 2003, 08:32:41
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 08:32:07 ; Search time 80 Seconds

(without alignments)
466,182 Million cell updates/sec

Title: US-09-937-555a-2

Perfect score: 997
Sequence: 1 EGDYSLCOOREKRLDDMRM.....DYGAGVTCDDDMONLCLG 181

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_Archea:*
2: SP_Bacteria:*
3: SP_Fungi:*
4: SP_Human:*
5: SP_Invertebrate:*
6: SP_Mammal:*
7: SP_Mhc:*
8: SP_Oxigenelle:*
9: SP_Plagie:*
10: SP_Plant:*
11: SP_Rodent:*
12: SP_Virus:*
13: SP_Vertebrate:*
14: SP_Unclassified:*
15: SP_Virus:*
16: SP_Bacteriap:*
17: SP_Archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	997	100.0	181	5	Q962V9
2	290	29.1	274	5	Q16969
3	264.5	26.5	424	5	Q16969
4	264.5	26.5	424	5	Q16969
5	262	26.3	218	5	Q77221
6	261.5	26.2	425	5	Q77153
7	216.5	21.7	465	5	Q9B1P2
8	209.5	21.0	459	5	Q9B1P2
9	209.5	21.0	459	5	Q9B1P2
10	208	20.8	491	5	Q9B1P2
11	207.5	20.8	491	5	Q9B1P2
12	190	19.1	425	5	Q19348
13	189.5	19.0	215	5	Q96317
14	187	18.8	220	5	Q44931
15	184	18.5	224	5	Q9GPN4
16	182	18.3	231	5	Q9B1Q7

17	180	18.1	248	5	Q9B1Q6	Q9B1Q6 cooperia pu
18	178	17.9	248	5	Q9B1Q8	Q9B1Q8 cooperia pu
19	178	17.9	489	11	Q9UJ56	Q9UJ56 mus musculu
20	178	17.9	489	11	Q9ET66	Q9ET66 mus musculu
21	167	16.8	208	5	Q9NSN4	Q9NSN4 caenorhabd1
22	159	15.9	415	4	Q8TCB8	Q8TCB8 homo sapien
23	158	15.8	500	4	Q9H336	Q9H336 homo sapien
24	157	15.7	220	5	Q9UB03	Q9UB03 wuchereria
25	156	15.6	220	5	Q97149	Q97149 wuchereria
26	154.5	15.5	207	5	Q20608	Q20608 caenorhabd1
27	153	15.3	213	5	Q93747	Q93747 caenorhabd1
28	152	15.2	212	5	Q20609	Q20609 caenorhabd1
29	152	15.2	220	5	Q16854	Q16854 onchocerca
30	148	14.8	188	11	Q9Z0U6	Q9Z0U6 rattus norv
31	148	14.8	220	5	Q44932	Q44932 brugia mala
32	146.5	14.7	208	5	Q18543	Q18543 caenorhabd1
33	143.5	14.4	246	5	Q9N313	Q9N313 caenorhabd1
34	143	14.3	207	5	Q93746	Q93746 caenorhabd1
35	142	14.2	210	5	Q18540	Q18540 caenorhabd1
36	141	14.1	117	5	Q9N591	Q9N591 heterodera
37	141	14.1	208	5	Q9N593	Q9N593 caenorhabd1
38	141	14.1	221	5	Q18347	Q18347 dirofilaria
39	140.5	14.1	211	5	Q18549	Q18549 caenorhabd1
40	140.5	14.1	332	11	Q9C035	Q9C035 mus musculu
41	140	14.0	424	11	Q9Z0K3	Q9Z0K3 mus musculu
42	139	13.9	262	5	Q22821	Q22821 caenorhabd1
43	138.5	13.9	209	5	Q18539	Q18539 caenorhabd1
44	137.5	13.8	209	5	Q18538	Q18538 caenorhabd1
45	135	13.5	203	4	Q9H108	Q9H108 homo sapien

ALIGNMENTS

RESULT 1

Q962V9	PRELIMINARY:	PRT:	181 AA.
AC	Q962V9		
DR	01-DEC-2001 (TREMBLREL. 19, Created)		
DR	01-DEC-2001 (TREMBLREL. 19, Last sequence update)		
DR	01-JUN-2002 (TREMBLREL. 21, Last annotation update)		
DE	Platelet Inhibitor (Fragment).		
GN	HPI.		
OS	Ancylostoma caninum (Dog hookworm).		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;		
OC	Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.		
OX	NCBI_TaxID=29170;		
RN	[1]		
RP	SEQUENCE FROM N. A.		
RA	DeValle A. Harrison L.M., Cappello M.;		
RT	*Cloning of the hookworm platelet inhibitor (HPI) from adult		
RT	Ancylostoma caninum.		
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF399709; AAK61732.1; ..		
DR	InterPro: IPR001283; Allrgn_V5/TPx1.		
DR	ProDom: PD000542; Allrgn_V5/TPx1; 1.		
FT	NOI_TER		
SO	SEQUENCE		
	181 AA: 20333 MW; FBSCED6FE567DNA CRC64;		
	Query Match		
	Best Local Similarity	100.0%;	Score 997; DB 5; Length 181;
	Matches	181; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	EGDYSLCOOREKRLDDMRMRETFELHNGYRAAFARNTSKMTMYDCTLEKAYKSAEK	60
DB	1	EGDYSLCOOREKRLDDMRMRETFELHNGYRAAFARNTSKMTMYDCTLEKAYKSAEK	60
QY	61	CSSEESSEENVDFSAATINIPLEAGNSMSEIFELRGKYVKNKGNSTANVWMSHD	120
DB	61	CSSEESSEENVDFSAATINIPLEAGNSMSEIFELRGKYVKNKGNSTANVWMSHD	120
QY	121	KLGCAVYVCSGKTHVCOYGPAPKDGKTIYEGAPCSRSDYGGVTCDDDMONLCLG	180
DB	121	KLGCAVYVCSGKTHVCOYGPAPKDGKTIYEGAPCSRSDYGGVTCDDDMONLCLG	180

DB 121 KIGCANVDCSGKTHVCGYGFPEAKGDKITYEGAPCSKSDYAGVCTDDMNLICIG 180
 QY 181 H 181
 DB 181 H 181

RESULT 2

ID 016969 PRELIMINARY: PRT: 274 AA.

AC 016969;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Neutrophil inhibitory factor precursor.
 GN NIF.
 OS Ancylostoma caninum (Dog hookworm).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
 OC Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
 OX NCBI_TaxID=29170;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HOMOGENATE;
 RX MEDLINE=94193581; PubMed-7908286;
 RA Moyle M., Foster D.L., McGrath D.E., Brown S.M., Laroche Y.,
 de Meuter J., Stanssens P., Bogowitz C.A., Friedl V.A., Ely J.A.,
 Soule H.R., Vlasuk G.P.;
 RT "A hookworm glycoprotein that inhibits neutrophil function is a ligand
 of the integrin CD11b/CD18.";
 RL J. Biol. Chem. 269:18008-10015(1994).
 DR EMBL: L27427; F00283; F00283; F00283; F00283; F00283; F00283;
 DR Interpro: IP00542; Allrgn_V5/Tpx1; 1.
 DR SMART: SM00198; SCP; 1.
 FT CHAIN 1 17
 FT SIGNAL 18 274
 FT CHAIN 18 274
 FT SIGNAL 18 274
 SO SEQUENCE 274 AA; 30680 MW; 51580873068DC7E CRC64;

Query Match 29.1%; Score 290; DB 5; Length 274;

Best Local Similarity 34.3%; Pred. No. 4.4e-19;

Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;

QY 14 DDDREMFTELHNGYRPAFAFARY-----KTSKRTWYDCTL 50
 DB 35 NDSRIQFLAMHNGYRSLALGHISITSESEDDDDGFLDPFAPRAKRYLEYDCEA 94
 QY 51 EKKAKVSKKCESE---PSEENVDFSAATLNI---PLEAGNSWSEIFEL-----R 98
 DB 95 EKSAYMSARNCSDSSPPEGYDENKTYIPENSN-NISEALAKAMISNAKEAFNLKRTGE 153
 QY 99 GKYVKNKNTSNINANVWDSHDKLCAVVD-----SGKT-----HYVCOYGE 142
 DB 154 GVLVRSNIDISNFMANLAMDAREKFCACAVVNCPLGEIDDETNDGELYATITIHVCHYFKI 213
 QY 143 AKGDGKTYEGAPCSKSDY 163
 DB 214 NKTGQPIYKVGTPCDDCSKY 234

RESULT 3

ID 076744 PRELIMINARY: PRT: 424 AA.

AC 076744;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Ancylostoma secreted protein 1 precursor.
 GN ASP1.
 OS Necator americanus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
 OC Ancylostomatidae; Ancylostomatidae; Bunostominae; Necator.
 OX NCBI_TaxID=510311;

RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=SHANGHAI;
 RX MEDLINE=96215086; PubMed-8636085;
 RA Hawdon J.M., Jones B.F., Hoffman D.R., Hotez P.J.;
 RT "Cloning and characterization of Ancylostoma-secreted protein. A novel
 protein associated with the transition to parasitism by infective
 hookworm larvae.";
 RT J. Biol. Chem. 271:6672-6678(1996).

RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=SHANGHAI;
 RX MEDLINE=8915177;
 RA Bin L., Hawdon J., Qiang S., Hainan R., Huiqing Q., Wei H.,
 Shu L., Xiang L., Xing F., Zheng F., Hotez P.;
 RA Ancylostoma secreted protein 1 (ASP-1) homologues in human
 hookworms.";
 RT Mol. Biochem. Parasitol. 98:143-149(1999).
 DR EMBL: AF079521; AAD3340.1; -;
 DR HSSP: P04284; 1CFE.
 DR Interpro: IP001283; Allrgn_V5/Tpx1.
 DR Pfam: PF00188; SCP; 1.
 DR PRINTS: P00837; V5TPXLIKE.
 DR PRODOM: PD000542; Allrgn_V5/Tpx1; 2.
 DR SMART: SM00198; SCP; 2.
 FT SIGNAL 18 424
 FT CHAIN 19 424
 FT SIGNAL 19 424
 SO SEQUENCE 424 AA; 45742 MW; BF1EB2P95F9B49F CRC64;

Query Match 26.5%; Score 264.5; DB 5; Length 424;

Best Local Similarity 32.5%; Pred. No. 1.8e-16;

Matches 62; Conservative 27; Mismatches 71; Indels 31; Gaps 6;

QY 7 CQGREKIDDDMEFTELHNGYRPAFAFARY-----KTSKRTWYDCTLEKAYK 56
 DB 227 CPSNTMTDSVADPFLSVHNEFSVAKRLEPDALGNAKRAKAKMYDDEVASAIR 286
 QY 57 SAERKCEPSSSE---NDVFSATLNI---PLEAGNSWSEIFEL-----LRG 99
 DB 287 HGKNCYQSHSEDPGLGENTIKTSYLKFDKNKAQASQAMNLEKEVGSPNSVLT 346
 QY 100 KYVNR-NGKTSNINANVWDSHDKLCAVVDSCGKTHVCGYGFPEAKGDKITYEGAPCS 158
 DB 347 ALMNRPMQIGHYOTAMADITYKLCAVVPFNDPTFGVCOYRPGCNMGHVIYTMGPCS 406
 QY 159 RCDYGAAYTC 169
 DB 407 QCS---PGATC 414

RESULT 4

ID 09XZ41 PRELIMINARY: PRT: 424 AA.

AC 09XZ41;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Ancylostoma secreted protein 1 precursor.
 OS Ancylostoma caninum (Dog hookworm).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
 OC Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
 OX NCBI_TaxID=29170;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SHANGHAI;
 RX MEDLINE=20163524; PubMed-10701589;
 RA Shan Q., Zhan B., Xiao S.-H., Feng Z., Hotez P., Hawdon J.M.;
 RT "Variation between ASP-1 molecules from Ancylostoma caninum in China
 and the United States.";
 RT J. Parasitol. 86:181-185(2000).
 DR EMBL: AF132291; AAD31839.1; -;
 DR HSSP: P04284; 1CFE.


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DR InterPro: IPR001283; Allrgn_v5/Tpx1.
DR Pfam: PF00188; SCP, 1.
DR PRINTS: PR00837; V5TPX1KE.
DR ProDom: PD000542; Allrgn_v5/Tpx1; 2.
DR SMART: SM00198; SCP, 2.
FW Signal.
FT CHAIN 1 18 POTENTIAL.
SQ SEQUENCE 424 AA; 45761 MW; 8409CDF8AEDCD248E CRC64;

Query Match 26.5%; Score 264.5; DB 5; Length 424;
Best Local Similarity 32.5%; Pred. No. 1.8e-16;
Matches 62; Conservative 27; Mismatches 71; Indels 31; Gaps 6;

OY 7 COOREKLDDBREMTLHNGYRAFAFARNY-----KTSKRTWYVDCLEEKAYK 56
DB 227 CPSNTGMTDSVDRDTFLSHNEFRSSVARGLEPDALGNAAPKAAKILKKVYDCVEASAIR 286
OY 57 SAEKSESPSESEE-----NVDFSAATLNI-----PLEAGNSWSEIFE-----LRG 99
DB 287 HGNCVYQHSHGDRGLGENIKTSYVAKFKKNAKAKQSOLMMELKEYGVSNNLT 346
OY 100 KYVK-KGTSNINAMWDSHKLCAYVDCSGKTHVYCYGPEAKGDKTIYEGAPCS 158
DB 347 ALMKRPMQIGHTTQAMDTTYKLCAYVFCNDFTGVCQYGPGGNYMGVITYMGOPCS 406
OY 159 RCDSDYAGATC 169
DB 407 QCS---PGATC 414

RESULT 5
OY 077221 PRELIMINARY; PRT; 218 AA.
AC 077221:
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Secreted protein ASP-2 precursor.
GN ASP-2.
OS Ancylostoma caninum (Dog hookworm).
OC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Strongylida;
OC Ancylostomatoidae; Ancylostomatidae; Ancylostominae; Ancylostoma.
OX NCBI_TaxID=29170;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALTIMORE;
RC MEDLINE-99270306; PubMed-10340481;
RA Hawdon J.M., Nattasinhan S., Hoter P.J.;
RT Ancylostoma secreted protein 2: cloning and characterization of a
RT second member of a family of nematode secreted proteins from
RT Ancylostoma caninum.
RL Mol. Biochem. Parasitol. 99:149-165(1999).
DR HSP, P04284; ICFE.
DR InterPro: IPR001283; Allrgn_v5/Tpx1.
DR Pfam: PF00188; SCP, 1.
DR PRINTS: PR00837; V5TPX1KE.
DR ProDom: PD000542; Allrgn_v5/Tpx1; 1.
DR SMART: SM00198; SCP, 1.
DR PROSITE: PS01009; SCP_AGS_PRL_SCT_1; 1.
FW Signal.
FT CHAIN 1 18 POTENTIAL.
SQ SEQUENCE 218 AA; 23954 MW; 8C263DEA808AA6F CRC64;

Query Match 26.3%; Score 262; DB 5; Length 218;
Best Local Similarity 30.4%; Pred. No. 1.3e-16;
Matches 58; Conservative 38; Mismatches 69; Indels 26; Gaps 5;

OY 13 LDDMKREMTLHNGYRAFAFARNY-----KTSKRTWYVDCLEEKAYKSGS 62
DB 27 MTEDAKQKFLVDHNSYRSMVAKGQAKDAISGNAPFAAKKKKLTIDCAVESTANQNAKCV 86

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OY 63 EEPSESE---ENVDFSAATLNI-----PLEAGNSWSEIFE-----ELGKYNNKGT 108
DB 87 FAHSHRGVGENEMTSTRQMDKAAQAQASDGMFSELAKTYGOENKLTITOLANNGVNI 146
OY 109 SNINAMWDSHKLCAYVDCSGKTHVYCYGPEAKGDKTIYEGAPCSRSDYAGVT 168
DB 147 GHYQWQWQESKICLCYENKSSMTYGVCIYSPQNMNNSLITKGNPCTKIDSDCSNNS 206
OY 169 CDDDMQWLACI 179
DB 207 CSAG--EALCV 215

RESULT 6
OY 077153 PRELIMINARY; PRT; 425 AA.
AC 077153:
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ancylostoma-secreted protein 1 precursor.
GN Asp1.
OS Ancylostoma duodenale.
OC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Strongylida;
OC Ancylostomatoidae; Ancylostomatidae; Ancylostominae; Ancylostoma.
OX NCBI_TaxID=51022;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SHANGHAI;
RC MEDLINE-96215086; PubMed-8636085;
RA Hawdon J.M., Jones B.F., Hoffman D.R., Hoter P.J.;
RT Cloning and characterization of Ancylostoma-secreted protein. A novel
RT protein associated with the transition to parasitism by infective
RT hookworm larvae.
RL J. Biol. Chem. 271:6672-6678(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SHANGHAI;
RC MEDLINE-9915177;
RA Bin Z., Hawdon J., Qiang S., Hainan R., Huang Q., Wei H.,
RA Shu Hua X., Fienha L., Xing G., Zheng F., Hoter P.;
RT Ancylostoma secreted protein 1 (ASP-1) homologues in human
RT hookworms.
RL Mol. Biochem. Parasitol. 98:143-149(1999).
DR EMBL, AF074802; AAD1339.1; -.
DR InterPro: IPR001283; Allrgn_v5/Tpx1.
DR Pfam: PF00188; SCP, 1.
DR PRINTS: PR00837; V5TPX1KE.
DR ProDom: PD000542; Allrgn_v5/Tpx1; 2.
DR SMART: SM00198; SCP, 2.
FW Signal.
FT CHAIN 1 19 POTENTIAL.
SQ SEQUENCE 425 AA; 45821 MW; 1F6B9D7E62EEDDAB CRC64;

Query Match 26.2%; Score 261.5; DB 5; Length 425;
Best Local Similarity 33.5%; Pred. No. 3.4e-16;
Matches 64; Conservative 23; Mismatches 73; Indels 31; Gaps 6;

OY 7 COOREKLDDBREMTLHNGYRAFAFARNY-----KTSKRTWYVDCLEEKAYK 56
DB 228 CPSNTGMTDSVDRDTFLSHNGFRSSVARGLEPDALGNAAPKAAKILKKVYDCVEASAIR 287
OY 57 SAEKSESPSESEE-----ENVDFSAATLNI-----PLEAGNSWSEIFE-----LRG 99
DB 288 HGNCVYQHSHGDRGLGENIKTSYVAKFKKNAKAKQSOLMMELKEYGVSNNLT 347
OY 100 KYVK-KGTSNINAMWDSHKLCAYVDCSGKTHVYCYGPEAKGDKTIYEGAPCS 158
DB 348 ALMKRPMQIGHTTQAMDTTYKLCAYVFCNDFTGVCQYGPGGNYMGVITYMGOPCS 407
OY 159 RCDSDYAGATC 169

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DB      408 GCA---ATATC 415

RESULT 7
ID      0981P2      PRELIMINARY;      PRT;      465 AA.
AC      0981P2;
DT      01-JUN-2001 (TREMBLrel. 17, Created)
DT      01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Activation associated secreted protein-like protein (Fragment).
OS      Cooperia punctata.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC      Trichostrongylidae; Cooperiidae; Cooperia.
OX      NCBI_TaxID=96640;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CP-ASP-1B;
RA      Yacuda A.P., Eysker M., Vieira Bressan M.C.R., De Vries E.;
RT      "Analysis of a family of activation associated secreted protein (ASP)
RT      homologs of Cooperia punctata."
RT      Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF352714; AKK3199.1; -.
DR      HSSP; P04284; 1CFE.
DR      InterPro; IPR001283; Allrgn_V5/TpX1.
DR      Pfam; PF00188; SCP; 1.
DR      PRINTS; PR00837; V5TPXLIKE.
DR      ProDom; PD000542; Allrgn_V5/TpX1; 2.
DR      SMART; SM00198; SCP; 1.
DR      NON_TER
SQ      SEQUENCE 465 AA; 51628 MW; F00F886C2A99993A CRC64;

Query Match 21.7%; Score 216.5; DB 5; Length 465;
Best Local Similarity 27.8%; Pred. No. 5.9e-12;
Matches 57; Conservative 30; Mismatches 79; Indels 39; Gaps 7;

OY      5 SLCOQREKIDDDMREMTLHNGYRAAFARNY-----RTSKRTMYDCTLEEK 53
DB      15 ALLSLNNGTDEVRILFLDKHNEVRSYIAKGAQNPVPGVNGTSTRAALMLVRIODEVED 74
OY      54 AYKSAE-KCSEPPSEEE-----NVDFSAATLNIPLDAGNSWSEITELNG- 99
DB      75 MMTMAQOCAYAPFESDKHYGRNTWGMGIPNKTAAESSV-----DWFED---ELRSY 126
OY      100 -----IVYKKNKTSNTIANWYDSHDKLCAVVDSCGKTHVVCQYGEAKGDGKTYEG 154
DB      127 GVPDNRKTYRNIDAVDYSQWYQWYKIGCVVASCSSMTWVACGSPAGNIDGSLIYELG 186
OY      155 APCSRCSDDGAGVCTDDDMQNLICI 179
DB      187 DPCMKNECKC-TNCTCKGKALCI 210

RESULT 8
ID      018519      PRELIMINARY;      PRT;      222 AA.
AC      018519;
DT      01-JAN-1998 (TREMBLrel. 05, Created)
DT      01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      24 kDa excretory/secretory protein.
DE      Haemonchus contortus (Barber pole worm).
OS      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC      Trichostrongylidae; Haemonchidae; Haemonchinae; Haemonchus.
OX      NCBI_TaxID=6289;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      MEDLINE=97418804; PubMed=9274880;
RA      Schallig H.D., van Leeuwen M.A., Verstegen B.E., Cornelissen A.W.;
RT      "Molecular characterization and expression of two putative protective
RT      excretory secretory proteins of Haemonchus contortus."
RT      Mol. Biochem. Parasitol. 88:203-213(1997).

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DR      EMBL; U64793; AAC4714.1; -.
DR      InterPro; IPR001283; Allrgn_V5/TpX1.
DR      Pfam; PF00188; SCP; 1.
DR      PRINTS; PR00837; V5TPXLIKE.
DR      ProDom; PD000542; Allrgn_V5/TpX1; 1.
DR      SMART; SM00198; SCP; 1.
DR      PROSITE; PS01009; SCP_AGS_PRL_SCP_1; 1.
SQ      SEQUENCE 222 AA; 24633 MW; 37B8840ED83100D8 CRC64;

Query Match 21.5%; Score 214; DB 5; Length 222;
Best Local Similarity 28.0%; Pred. No. 4.1e-12;
Matches 58; Conservative 28; Mismatches 89; Indels 32; Gaps 8;

OY      2 GDYSLCOQREKIDDDMREMTLHNGYRAAFARNY-----RTSKRTMYDCT 49
DB      17 GHASWCPPTNGMSDEVRQGFVNKNHNAVRLVAKGEAKNAKEIGYAPFAAHLKYVDCA 76
OY      50 LERKAYKSAEKC--SEPPSEEE--VDVFSATLN-----IPLEAGNSWSEITELRG 100
DB      77 IENYMANFAKCVFAHNSYSESNMNGOYLWYTSILNOKTVAAASVDLWFDL-QONGV 135
OY      101 VYK-----NKTSTIANWYDSHDKLCAVVDSCGKTHVVCQYGEAKGDGKTYEE 153
DB      136 PVDNMTMAVFNRRGTHYGYQWYQWYKIGCVVASCSSMTWVACETDSAGVYKMPLEYE 195
OY      154 GPCSRCSDDG-AGVCTDDDMQNLICI 179
DB      196 GNPCTNNECKCITNCTCKGKALCI 220

RESULT 9
ID      P09058      PRELIMINARY;      PRT;      246 AA.
AC      P09058;
DT      01-MAY-1997 (TREMBLrel. 03, Created)
DT      01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      T05A10.5 protein.
DE      T05A10.5.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC      Rhabditidae; Pelodierinae; Caenorhabditis.
OX      NCBI_TaxID=6239;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      Suston J.E.;
RA      Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN      121
RP      MEDLINE=99069613; PubMed=9851916;
RX      SEQUENCE FROM N.A.
RT      none;
RT      "Genome sequence of the nematode C. elegans: A platform for
RT      investigating biology."
RT      Science 283:2012-2018(1998).
DR      EMBL; Z68108; CAN92136.1; -.
DR      HSSP; P04284; 1CFE.
DR      InterPro; IPR001283; Allrgn_V5/TpX1.
DR      Pfam; PF00188; SCP; 1.
DR      PRINTS; PR00837; V5TPXLIKE.
DR      ProDom; PD000542; Allrgn_V5/TpX1; 1.
DR      SMART; SM00198; SCP; 1.
SQ      SEQUENCE 246 AA; 27956 MW; FB5770261350DE54 CRC64;

Query Match 21.0%; Score 209.5; DB 5; Length 246;
Best Local Similarity 27.2%; Pred. No. 1.2e-11;
Matches 59; Conservative 26; Mismatches 87; Indels 45; Gaps 7;

OY      6 LCOQREKIDDD-----MREMTLHNGYRAAFARNY-----RTSK 40
DB      29 LQAASMYKDDGSGFOCDNSLVSVTRNFTLEQHNFYRSLAAGFEMNGETNTSQPASQ 88
OY      41 MNTMYDCTLEEKYKSAEKC-----SEPPSEEEVDVFSAT-----LNPPLDAGNSW 91

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DB 89 MIKREYDCEMFERROKMANNCVFAHSAHYERPNONGNLTMSFSPDPRSLIHTAVEKMW 148
OY 92 SEIFE-----LRKYVKNKGT-SNIAMVWDSHDLGCAVYDSCGKTHVCOXGPE 142
DB 149 CELEFEGTPIIDVLTPELWDLGKRAIGHYQGMAMDRYLLGCGINCPKMSYVCHYGRFA 208
OY 143 AKGCGKTYEEGAPSCRCSDYAGVTCDDQMNLCI 179
DB 209 GNRKNNKTYEIGDPCVDDCDIGTDCER--TTSICV 243

RESULT 10
ID 045132 PRELIMINARY; PRT; 459 AA.
AC 045132;
DB 01-JUN-1998 (TREMBLrel. 06, Created)
DB 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DB 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative secretory protein precursor.
GN HC40.
OS Haemochus contortus (Barber pole worm).
OC Eukaryota; Metazoa; Chromadorea; Rhabdilitida; Strongylida;
OC Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
OX NCBI_Taxid=6289;
RN [1]
RP SEQUENCE FROM N.A.
RA Rehman A., Jaamer D.P.;
RL Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF047417; AAC03562.1;
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR PRODOM: PD000542; Allrgn_V5/Tpx1; 2.
DR SMART: SM00198; SCP; 2.
DR SIGNAL.
KV SIGNAL.
FT CHAIN 1 18 POTENTIAL.
FT SIGNAL 19 459 POTATIVE SECRETORY PROTEIN.
SQ SEQUENCE 459 AA; 50924 MW; 88FAC09A01FC57B CRC64;

Query Match 20.98; Score 208; DB 5; Length 459;
Best Local Similarity 28.58; Pred. No. 3,6e-11;
Matches 57; Conservative 36; Mismatches 74; Indels 28; Gaps 8;

OY 13 LDDNREHFEHLNGYRAAFAARN-----KTSKRTMYDCTLEKAYKAERCS 62
DB 267 MIDEAKMFVDKNEHNSLAKGQAKRGQAFAPAAAMKVNDDCVANMMSKTCI 326
OY 63 EEPSESE-----ENVDFSAATLN---IPFAGSMSEIFEL---RKYVKNKGT-- 108
DB 327 FGLNTAAMLAKRGNMNMMSKANNTTEAARAVAMFGDLOKGVPENNVFTMAYTTL 386
OY 109 SNIAMVWDSHDLGCAVYDSCGKTHVCOYGPAPKAGDKTYEEGAPSCRCSDYGA-G 166
DB 387 SKISQALWSSDRICQVYPCWMSMTVYCEINPGDGLPSALITVDVDDPTDADOCQPG 446
OY 167 VTGDDDMQNLICI 179
DB 447 CTCGRD--EALCV 457

RESULT 11
ID 098104 PRELIMINARY; PRT; 491 AA.
AC 098104;
DB 01-JUN-2001 (TREMBLrel. 17, Created)
DB 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DB 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Activation associated secreted protein-like protein (Fragment).
OS Cooperia punctata.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Strongylida;
OC Trichostrongyloidea; Cooperiidae; Cooperia.
OX NCBI_Taxid=56640;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-CP-ASP-1A;
RA Yatsuda A.P., Eysker M., Vleira Bressan M.C.R., De Vries E.;
RT "Analysis of a family of activation associated secreted protein (ASP)
RL homologs of Cooperia punctata."
DB Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF352702; AA35187.1;
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR InterPro: IPR002965; P-rich_extensn.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PRO1217; PRICHEXTENS.
DR PRODOM: PD000542; Allrgn_V5/Tpx1; 2.
DR SMART: SM00198; SCP; 2.
DR PROSITE: PS01009; SCP_AGS_PRL_SCT_1; 1.
FT NON_TER 1
SQ SEQUENCE 491 AA; 55244 MW; 25B9B435E613857E CRC64;

Query Match 20.88; Score 207.5; DB 5; Length 491;
Best Local Similarity 28.98; Pred. No. 4,4e-11;
Matches 57; Conservative 30; Mismatches 85; Indels 25; Gaps 8;

OY 6 LCQGRKLDNREHFEHLNGYRAAFAARN-----YKTSKRTMYDCTLEKAA 54
DB 12 TCSLNSMTVYIKRITLDNHNHSLVLRGAKDPRGTGOTIPKATRLMKSYDCEADVYA 71
OY 55 YKSNF-KC--SEEPSSEENVDFSAATLNIP--EAGNS---HWSEIFEL---RKYV 103
DB 72 MNMVAQACTYARKSKKRYNNTNGICIRFNKKAESYVDNFNIRYGVPRDMYT 131
OY 104 KNGKTSNIAMVWDSHDLGCAVYDSCGKTHVCOYGPAPKAGDKTYEEGAPSCRCSDY 163
DB 132 RDTSVHSGIIMQDSYKIGCAVAMCQSMTWACAVNPAGNNYSGQIYEQEPCKRNOCD 191
OY 164 GA-GVTCDDDMQNLICI 179
DB 192 KNCQCTCT--TESLCT 206

RESULT 12
ID 019348 PRELIMINARY; PRT; 425 AA.
AC 019348;
DB 01-NOV-1996 (TREMBLrel. 01, Created)
DB 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DB 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE FilC7.3 protein.
GN FilC7.3 OR VAP-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;
OC Rhabdilitidae; Pelodierinae; Caenorhabdilitis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RC MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnscoough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Fulton L.,
RA Craixton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kerhaw J., Kirsten J., Laister N., Laister B., Lathrop M.,
RA Lightning J., Lloyd C., Murray A., Mortimore B., O'Brien P., O'Brien M.,
RA Parsons N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Therry-Mieg J., Thomas K., Vaughan K., Vaughan K., Watson R.,
RA Watson A., Welnsstock L., Wilkinson-Spoat J., Wolfdman P., III of C.
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RL elegans."
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RA Tatch A., Vetter J.;

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RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RC SEQUENCE FROM N.A.
 RA STRAIN-N2 BRISTOL;
 RL Liu T.X.;
 DR Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U42839; AAC69015.1;
 DR EMBL; AF112356; AAD27559.1;
 DR InterPro; IPR001283; Allrgn_V5/TpX1.
 DR InterPro; IPR001230; Prenyl_site.
 DR Pfam; PF00188; SCP; 1.
 DR PRINTS; PR00837; V5TPXLIKE.
 DR ProDom; PD000542; Allrgn_V5/TpX1; 2.
 DR SMART; SM00198; SCP; 2.
 DR PROSITE; PS00294; PRENYLATION; UNKNOWN; 1.
 DR PROSITE; PS00294; PRENYLATION; UNKNOWN; 1.
 SQ SEQUENCE 425 AA; 46323 MW; 9E7233B8A7340EEB CRC64;

Query Match 19.1%; Score 190; DB 5; Length 425;
 Best Local Similarity 23.0%; Pred. No. 1.6e-09;
 Matches 45; Conservative 40; Mismatches 79; Indels 33; Gaps 5;

QY 4 YSLCOORREKIDDMREKFTLHNGYRAAFARAYKTSK-----RTMYDCTL 50
 DB 222 FIMCPSYVDQDQARQNFQDTHNKLFTSLAKLEADGIAAGAFAPAKQMPLYVTSCTV 281
 QY 51 EEKAYKSEKSEPSSEEE-----NDVFSATLNIPL-----EAGNSWSEIFE----- 96
 DB 282 EAMRTMAKGLYOHSTSAORPELGSLMISINNMPLOTADBSKAMWSELDKDFGVGS 341
 QY 97 ---LRGKYNNKNGTSINAMVWDSDKIGCAVDCSGKTHVVOYGPBKAQDKTIYEE 153
 DB 342 DNILQVAFDRG--VGHYTMAMEGTTETGCEVENCPEFTYSVCQYGPAGNYMNLITRK 399

QY 154 GAFCSKCSDDYAGAVTC 169
 DB 400 GSPCTADADCCPTQTC 415

RESULT 13
 Q96317 PRELIMINARY; PRT; 215 AA.
 AC Q96317;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Vap-1.
 OS Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 CC Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
 OX NCBI_TaxID=51029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gao B., Allen R., Meier T., Davis E.L., Baum T.J., Husey R.S.;
 RT "Molecular characterization and expression of two venom allergen-like
 RT secretory proteins from Heterodera glycines";
 RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF974386; AAK60209.1; Allrgn_V5/TpX1.
 DR InterPro; IPR001283; Allrgn_V5/TpX1.
 DR InterPro; IPR001230; Prenyl_site.
 DR Pfam; PF00188; SCP; 1.
 DR ProDom; PD000542; Allrgn_V5/TpX1; 1.
 DR PROSITE; PS00294; PRENYLATION; UNKNOWN; 1.
 DR PROSITE; PS00294; PRENYLATION; UNKNOWN; 1.
 SQ SEQUENCE 215 AA; 23176 MW; FC200DDFCA8CB84 CRC64;

Query Match 19.0%; Score 189.5; DB 5; Length 215;
 Best Local Similarity 30.8%; Pred. No. 7.5e-10;
 Matches 53; Conservative 29; Mismatches 61; Indels 29; Gaps 9;

QY 25 HNGYRAAFAR---NYKTSKRT-----WVYDCTLEKAYKSEKSEPSSEEE---ENV 72
 DB 38 HNNYRQLAKGTADNKGKAPAGSNLQOKYDSNIESVAGNMGANGSMHSGSSSGMGT 97
 QY 73 DVSAAATL---NIPLEAGNSWSEI---FELRGKY-----YNNKNGTSINAMVWDSDK 121

DB 98 YMTSSSTISBADLKKACDMMWAEIKQFQSSILVDMQAFNRG--IGHSQQAAMSTAO 155
 QY 122 LGCAVVC-----SGKTHVVOYGPBKAQDKTIYEEGAPSCSDYAGAVTCD 170
 DB 156 IGCAMARCPSTWYVYCNKYKANGFNLPYVYKGAACSKSDYN-GATCD 206

RESULT 14
 O44931 PRELIMINARY; PRT; 220 AA.
 ID O44931;
 AC O44931;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Vespid allergen antigen homolog.
 OS Onchocerca volvulus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Splurida; Filarioidea;
 CC Onchocercidae; Onchocerca.
 OX NCBI_TaxID=6282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McCarthy J.S., Hopkins R.M.;
 RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF042087; AAB97282.1;
 DR HSSP; P04284; ICEE.
 DR InterPro; IPR001283; Allrgn_V5/TpX1.
 DR Pfam; PF00188; SCP; 1.
 DR ProDom; PD000542; Allrgn_V5/TpX1; 1.
 DR SMART; SM00198; SCP; 1.
 DR SMART; SM00198; SCP; 1.
 SQ SEQUENCE 220 AA; 24831 MW; 99C3232D74264052 CRC64;

Query Match 18.8%; Score 187; DB 5; Length 220;
 Best Local Similarity 27.9%; Pred. No. 1.3e-09;
 Matches 55; Conservative 29; Mismatches 63; Indels 50; Gaps 10;

QY 10 REKIDDMREKFTLHNGYRAAFAR-NY-----KTSKRTVYDCTLEKAYKSAE 59
 DB 21 RGLTSLQORDIIVDEHNKYSRLVGNFANKDGNLMPKCKNMMEKCELEISAQWMD 80
 QY 60 KC--SEPSSEEE-----NDVFSATLNIPLKNGNSWSEIFEELGKAYK 104
 DB 81 QCTGYSPEHQRGVGENITVALGLPKDVEFNLSALFAIE---SWTEL--IKSYRNP 135

QY 105 NGR-TSNIAN-----WVWDSDKIGCAV---DCSGKTHVVOYGPBKAQDKTIYEE 152
 DB 136 SKLTSVYASQDYLHRTQAMAKGTHKYGCGIAMHCDGGAFTVCHYAPRNTIGELIYE 195

QY 153 BGARC-----SRCS 161
 DB 196 QSPCKYKHKCTRKCS 212

RESULT 15
 Q96PN4 PRELIMINARY; PRT; 224 AA.
 ID Q96PN4;
 AC Q96PN4;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Activation-associated secreted protein-2.
 GN ASP-2.
 OS Onchocerca volvulus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Splurida; Filarioidea;
 CC Onchocercidae; Onchocerca.
 OX NCBI_TaxID=6282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tave W., Pearlman E., Unnasch T.R., Lustigman S.;
 RT "Angiogenic activity of Onchocerca volvulus recombinant proteins
 RT similar to vespid venom antigen 5";

RL MBL Blochem Parasitol. 109:91-99(2000).
 DR EMBL AF315563; AAG40311.1;
 DR InterPro: IPR001283; Allrgn_V5/Tpx1.
 DR Pfam PF00188; SCP; 1.
 DR PRINTS: PR00837; V5TPXLIKE.
 DR ProDom: PD000542; Allrgn_V5/Tpx1; 1.
 DR SMART: SM00198; SCP; 1.
 SQ SEQUENCE 224 AA; 25253 MW; 8AF47A01522P5C3A CRC64;

Query Match 18.3%; Score 184; DB 5; Length 224;
 Best Local Similarity 30.3%; Pred. No. 2.6e-09;
 Matches 57; Conservative 20; Mismatches 73; Indels 38; Gaps 9;

QY 10 REKIDDDMRKEMTELNGYRAAFAR-NKTS-----KRTVYDCLEEKAYKSE 59
 DB 21 RGLKLPQYREKRYREHNRLRSKLAGTYKNSAGKMPKGNMKEKNCLELMAQRAD 80
 QY 60 KCSPEPSEEE-----NDVFSATLNIPLNGSNWSEIF-ELRGKVTN 103
 DB 81 GCVGNSPKDRGRIGENYTORSDTSVAYVGSIMALE---SWVVELRSTKKNPSR 137
 QY 104 K-----NGKTSNIAMVWDSHDKLGCAY-VDC-SGKTHV-VQYGPRAKDGKTIYEG 154
 DB 138 KYSIVANRGVSNFTQIANGKTKYVGGIATHCDDGGAFAVAVCOYINPGNTMSESIYEG 197
 QY 155 APCSRCD 162
 DB 198 RPKCTDND 205

RESULT 16

O9BI07 PRELIMINARY; PRT; 231 AA.
 AC O9BI07;

DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Activation associated secreted protein-like protein (Fragment).
 OS Cooperia punctata.
 OC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Strongylida;
 OC Trichostrongyloidea; Cooperiidae; Cooperia.
 NCBI_TaxID=96640;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CP-ASPVAR-5;
 RA Yatsuda A.P., Eysker M., Vieira Bressan M.C.R., De Vries E.;
 RT Analysis of a family of activation associated secreted protein (ASP)
 RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF352699; AAK35184.1;
 DR HSSP: P04284; ICPE.
 DR InterPro: IPR001283; Allrgn_V5/Tpx1.
 DR Pfam: PF00188; SCP; 1.
 DR PRINTS: PR00837; V5TPXLIKE.
 DR ProDom: PD000542; Allrgn_V5/Tpx1; 1.
 DR SMART: SM00198; SCP; 1.
 FT NON-TER 1
 SQ SEQUENCE 231 AA; 25824 MW; C5225C9AA17AAD00 CRC64;

Query Match 18.3%; Score 182; DB 5; Length 231;
 Best Local Similarity 26.6%; Pred. No. 4.1e-09;
 Matches 54; Conservative 27; Mismatches 86; Indels 36; Gaps 7;

QY 7 COOREKLDMDMRKEMTELNGYRAAFARNT-----KTSKRTVYDCLEEKAYK 57
 DB 32 CTANNGMTDQVAVQLDKHNEYRLVARGAONKGTGFAFKARHRLRYDCDLEAHVMEH 91
 QY 58 AEKCSPEPSS-----EENVDVSATLNIPLNGSNWSEIFELRGKVTN 103
 DB 92 VKTKCGHSPFVLKRGONIMATVPNLDKAAKRSV-----DMYIELTKYGITADN 146
 QY 104 K-----NGKTSNIAMVWDSHDKLGCAYVDC--SGKTHVQYGPRAKDGKTIYEGAP 156

DB 147 KISIDNAATGHYSQVWQKSNRLGCAVSCPEQRKLFVGEYLPNGNTLRHLIYDIGEP 206
 QY 157 CSRCSDYGAGVTCDDDMONLICI 179
 DB 207 CKRDECKCS-SCRCSTOLSMCI 228

RESULT 17

O9BI06 PRELIMINARY; PRT; 248 AA.
 AC O9BI06;

DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Activation associated secreted protein-like protein (Fragment).
 OS Cooperia punctata.
 OC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Strongylida;
 OC Trichostrongyloidea; Cooperiidae; Cooperia.
 NCBI_TaxID=96640;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CP-ASPVAR-5;
 RA Yatsuda A.P., Eysker M., Vieira Bressan M.C.R., De Vries E.;
 RT Analysis of a family of activation associated secreted protein (ASP)
 RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF352700; AAK35185.1;
 DR HSSP: P04284; ICPE.
 DR InterPro: IPR001283; Allrgn_V5/Tpx1.
 DR Pfam: PF00188; SCP; 1.
 DR PRINTS: PR00837; V5TPXLIKE.
 DR ProDom: PD000542; Allrgn_V5/Tpx1; 1.
 DR SMART: SM00198; SCP; 1.
 FT NON-TER 1
 SQ SEQUENCE 248 AA; 27528 MW; ABF932E60DB67411 CRC64;

Query Match 18.1%; Score 180; DB 5; Length 248;
 Best Local Similarity 26.1%; Pred. No. 6.8e-09;
 Matches 53; Conservative 28; Mismatches 86; Indels 36; Gaps 6;

QY 7 COOREKLDMDMRKEMTELNGYRAAFARNTKSK-----NRTVYDCLEEKAYK 57
 DB 49 CTIDNGMTDEARQVFLDKHNEYRLVARGAONKGTGLAPPAARLRLKRYDCDLEAHVMEH 108
 QY 58 AEKCSPEPSS-----ENVDVSATLNIPLNGSNWSEIFELRGKVTN 103
 DB 109 VAKCKGHSSTEDVYLRGONIMATVPNLDKAAKRSV-----DMYIELTKYGITADN 163
 QY 104 K-----NGKTSNIAMVWDSHDKLGCAYVDC--SGKTHVQYGPRAKDGKTIYEGAP 156
 DB 164 KISIDNAATGHYSQVWQKSNRLGCAVSCPEQRRLVYGCETWPGNTLRHLIYDIGEP 223
 QY 157 CSRCSDYGAGVTCDDDMONLICI 179
 DB 224 CKRDECKCS-SCRCSTOLSMCI 245

RESULT 18

O9BI08 PRELIMINARY; PRT; 248 AA.
 AC O9BI08;

DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Activation associated secreted protein-like protein (Fragment).
 OS Cooperia punctata.
 OC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Strongylida;
 OC Trichostrongyloidea; Cooperiidae; Cooperia.
 NCBI_TaxID=96640;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CP-ASPVAR-7;
 RA Yatsuda A.P., Eysker M., Vieira Bressan M.C.R., De Vries E.;

*Analysis of a family of activation associated secreted protein (ASP)
 RT homologs of Cooperia punctata.
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF352898; AKK3183.1;
 DR HSSP: P04284; ICPE.
 DR InterPro: IPR001283; Allrgn_V5/tpx1.
 DR Pfam: PF00188; SCP; 1.
 DR PRINTS: PR00837; V5TPXLIKE.
 DR PRODOM: PD000542; Allrgn_V5/tpx1; 1.
 DR SMART: SM00198; SCP; 1.
 FT NON_TER
 SQ SEQUENCE 248 AA; 27558 MW; A7ED083B9BEF7481 CRC64;

Query Match 17.9%; Score 178; DB 5; Length 248;
 Best Local Similarity 26.1%; Pred No. 18-08; 87; Indels 36; Gaps 6;
 Matches 53; Conservative

QY 7 COORELDDREMTLHNGYRAAFARNYTKS-----RRTVYDCTLEEKAYKS 57
 DB 49 CTLDNGMTBDAQVLDKHNRYQLVARGAQNKTGLAPPAARMLKRTYDCDLAHVMEH 108
 QY 58 AERCSSEBSEE-----ENDVPSAATLNIPLEAGNSWSEIFELRGKYNN 103
 DB 109 VAKCKGSHSPDYVLRGQGNIMATVYNLDKAAKRSV-----DMYFELRYGITADN 163
 QY 104 K-----NGTSMIANWMDSHDKGCAVYDC--SGTTHVCOYGEPAKSGKTYEEGAP 156
 DB 164 KISTDNATGTHYSGVYVQKSNRIGCAAVSCPEGRRLTYGCEYVPGGNTLRHLITYDIGEP 223
 QY 157 CSKCSGYGAGVCTDDQNTLCI 179
 DB 224 CKRDECKCS-SCRCSTLSMCI 245

RESULT 19
 ID 09J356 PRELIMINARY; PRT; 489 AA.
 AC 09J356;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE Cysteine-rich protease inhibitor.
 GN 1200009H1IRIK OR CRIP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jang J.S., Hahn Y., Chung J.H.;
 RT Identification of novel mouse cysteine-rich protease inhibitor
 RT gene."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB046537; BAB03398.1;
 DR HSSP: P04284; ICPE.
 DR MGD: MGI:1921366; 1200009H1IRIK.
 DR InterPro: IPR001283; Allrgn_V5/tpx1.
 DR Pfam: PF00188; SCP; 1.
 DR PRINTS: PR00837; V5TPXLIKE.
 DR PRODOM: PD000542; Allrgn_V5/tpx1; 1.
 DR SMART: SM00198; SCP; 1.
 DR PROSITE: PS01009; SCP_AGS_PRL_SC7_1; 1.
 DR PROSITE: PS01010; SCP_AGS_PRL_SC7_2; 1.
 KW Protease.
 SQ SEQUENCE 489 AA; 52676 MW; 01C207BE12E3C9D CRC64;

Query Match 17.9%; Score 178; DB 11; Length 489;
 Best Local Similarity 28.6%; Pred. No. 2,4e-08;
 Matches 53; Conservative 25; Mismatches 73; Indels 34; Gaps 9;
 QY 13 LDDDMREMTLHNGYRAAFARNYTKSMTVYDCTLEEKAYKSARKC-----SEPPSE 68
 DB 21 LTREDKQTMVDLHNGYRAOVSP--PASDMLQHRWDELAFAFAVAKCKVGHKNGRR 78

QY 69 EENDVPSAATLNIPLEAGNSWSEIFELRGKYNN-----KNGKTSNIANNWMDSHDK 121
 DB 79 GENLEAATDEGMVPLAVGN--WHEEHE---YNNFSTATCDPNMCGHYTVVMSKTER 132
 QY 122 LGCAVYDC-----SGKTH-VVCOYGEPAKSGKTYEEGAPCSKSDYAGVTCDDM 173
 DB 133 ICGSHFCETLQGEVANHLVNCYEPGPNVNGRKRPDGTGSCPCP---LGYSK----- 185
 QY 174 ONLTC 178
 DB 186 ENSLC 190

RESULT 20
 ID 09ET66 PRELIMINARY; PRT; 489 AA.
 AC 09ET66;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE Cysteine-rich protease inhibitor.
 GN CRIP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jang J.S., Hahn Y., Chung J.H.;
 RT Genomic structure of murine cysteine-rich protease inhibitor gene."
 RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB046538; BAB03453.1; JOINED.
 DR EMBL: AB046538; BAB03453.1;
 DR HSSP: P04284; ICPE.
 DR InterPro: IPR001283; Allrgn_V5/tpx1.
 DR Pfam: PF00188; SCP; 1.
 DR PRINTS: PR00837; V5TPXLIKE.
 DR PRODOM: PD000542; Allrgn_V5/tpx1; 1.
 DR SMART: SM00198; SCP; 1.
 DR PROSITE: PS01009; SCP_AGS_PRL_SC7_1; 1.
 DR PROSITE: PS01010; SCP_AGS_PRL_SC7_2; 1.
 KW Protease.
 SQ SEQUENCE 489 AA; 52664 MW; 01C2009712E3C76D CRC64;

Query Match 17.9%; Score 178; DB 11; Length 489;
 Best Local Similarity 28.6%; Pred. No. 2,4e-08;
 Matches 53; Conservative 25; Mismatches 73; Indels 34; Gaps 9;

QY 13 LDDDMREMTLHNGYRAAFARNYTKSMTVYDCTLEEKAYKSARKC-----SEPPSE 68
 DB 21 LTREDKQTMVDLHNGYRAOVSP--PASDMLQHRWDELAFAFAVAKCKVGHKNGRR 78
 QY 69 EENDVPSAATLNIPLEAGNSWSEIFELRGKYNN-----KNGKTSNIANNWMDSHDK 121
 DB 79 GENLEAATDEGMVPLAVGN--WHEEHE---YNNFSTATCDPNMCGHYTVVMSKTER 132
 QY 122 LGCAVYDC-----SGKTH-VVCOYGEPAKSGKTYEEGAPCSKSDYAGVTCDDM 173
 DB 133 ICGSHFCETLQGEVANHLVNCYEPGPNVNGRKRPDGTGSCPCP---LGYSK----- 185
 QY 174 ONLTC 178
 DB 186 ENSLC 190

RESULT 21
 ID 09NSN4 PRELIMINARY; PRT; 208 AA.
 AC 09NSN4;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)

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DE H10D18.4 protein.
GN H10D18.4.
OS Caenorhabditis elegans.
OC Eukaryotes; Metazoa; Nematoda; Chromadorea; Rhabdittida; Rhabdittidae;
OC Rhabdittidae; Pelodierinae; Caenorhabdittids.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT *Genome sequence of the nematode C. elegans a platform for
RT investigating biology. The C. elegans Sequencing Consortium.*;
RT Science 282:2012-2018(1998).
RL [2]
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX Madson C., Yin-Mollam A., Keppeler D.;
RT "The sequence of C. elegans cosmid H10D18.";
RT submitted (Mar-1999) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX Waterston R.;
RT Submitted (Mar-2000) to the EMBL/GenBank/DDBJ databases.
RL EMBL; AC006655; AAC39876.1; -.
DR InterPro; IPRO01283; Allrgn_V5/Tpx1.
PR Pfam; PF00188; VSP; 1.
DR PRINTS; PR00837; V5TPXLRK.
DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR SMART; SM00198; SCP; 1.
SQ SEQUENCE 208 AA; 22147 MW; 9F6B3BBEBA618BCF CRC64;

Query Match          16.8%; Score 167; DB 5; length 208;
Best Local Similarity 26.8%; Pred. No. 8,9e-08;
Matches 52; Conservative 22; Mismatches 58; Indels 62; Gaps 8

OY      23 ELHNVRPAAPR-NV-----KTSKRRTVYDCITFEAKYSKEKSEE----- 64
Db       28 DAHNNLRSAIAGSYAAAGTQEPSNKNKIWDYVAALAAAGTAEAGCPDDHSGSTYGEN 87
OY      65 -----PSEENNDVPSAATLTIPLEACNSWMSFEFLRGKYNNNGKTS----- 109
Db       88 LYSWSSSNAPSSLDKGVG-----ASNWSES-----FGYGTWTFTIDEAGFMT 132
OY     110 ---NIANKVWDSDHKLCANVDCSG-----KTHVGYCGPEAKGDGKITVEGAPFS 158
Db     133 GIGHAYTAAEAETSKIGCGIKNCGRKANKNMYKVAVYCOYDSAGNMADSLTYOGCHTCS 192
OY     159 RCSDYGAGVTCCDD 172
Db           ||: :| |
              ||: :| |
              ||: :| |
Db     193 ACSCE---DASCED 203

QUEST 22
O8TCB8 PRELIMINARY; PRT; 415 AA.
ID O8TCB8;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DS Hypothetical 45.2 kDa protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NC NCBI_TaxId=9606;
RN [1]
RP SPOUNCE FROM N.A.
RC TRISBP-LUNG;
RL Studtmittel (FESB-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; F0022359; AAA22359.1; -.
AN Hypothetical protein.
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SQ  NON-TER  1  15.9%  Score 159; DB 4; Length 415;
FT  415 AA; 45230 MW; 945069C1607D38E3 CRC64;

Query Match 15.9%; Score 159; DB 4; Length 415;
Best Local Similarity 28.6%; Pred. No. 1.2e-06;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9

13 LDDDMREHETLHNGYPAARFARNTKSKRMVYDCTLEKAKVSKERC---SPEPSSE 68
DB 35 LTDEERKLAVELNLHYRAQVSP-ASDMLHMRDEDELAFAAAYARCCVWCHNKNGRR 92
OY 69 EENVVYFSAATNLPLDAGNSMMSEFELDRKRYNKGKTSNIAN-----YDSDSK 121
DB 93 GENLRALIDDEMDPL-AMEWHNE-----KEHNLSAATCSGCMGCHYYVWAKTER 146
OY 122 IGCNAVVDG-----GKNV-----VCOYGEPAAGDCKITTEGACFSCSDYAGATCDDDW 173
DB 147 ICGSHFEKQGVETNIELVLCNTEPFGVAKRRPDRGTSQSCP---SGVHC--- 199
OY 174 QNLIC 178
DB 200 KNSLC 204

RESULT 23
O9H336 PRELIMINARY; PRT; 500 AA.
AC O9H336;
DT 01-MAR-2001 (TREMBLrel, 16, Created)
DT 01-MAR-2001 (TREMBLrel, 16, Last sequence update)
DE 01-JUN-2002 (TREMBLrel, 21, Last annotation update)
DE Putative secretory protein precursor (Cococriasp).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid-9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-AORTA;
RA Zhao Y., Cao H., Jiang Y., Meng X., Zhao X., Liu D., Ding J.;
RT "Cloning and characterization of a trypsin inhibitor-like protein gene
RT in human aorta.";
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-HEART, AND TESTIS;
RA Smith D.H., Collins-Racie L.A., Lavallie E.R., Gamer L., Roberts D.J.,
RA Mariso V.A., Copland N.G., Jenkins N.A., McCoy J., Tabin C.J.;
RT "A novel cysteine-rich secreted protein (CRISP) family member,
RT Cococriasp, provides insight into the process of septation in the
RT developing chicken midbrain.";
RL Submitted (Dec-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARY;
RA Strausberg R.;
RL Submitted (Jan-2002) to the EMBL/GenBank/DBJ databases.
RA EMBL: AF143573; AAC43287.1; -
DR EMBL: AF329197; AAK16495.1; -
DR EMBL: BC020514; AAH20514.1; -
DR HSSP: P04284; ICPE.
DR InterPro: IPR001283; Allgpn_V5/TpX1.
DR InterPro: IPR004043; LCCL_dom.
DR Pfam: PFO0188; SCP.1.
DR PRINTS: PRO0837; VSTPKLKE.
DR ProDom: PD000543; Allgpn_V5/TpX1.1.
DR SMART: SM00198; SCP.1.
DR PROSITE: PS01010; SCP_AGS_PRL_SCT.2.1.
SQ SEQUENCE 500 AA; 56888 MW; 203BDCDDDA003CB CRC64;

Query Match 15.8%; Score 158; DB 4; Length 500;
Best Local Similarity 25.5%; Pred. No. 1.8e-06;
Matches 53; Conservative 31; Mismatches 66; Indels 58; Gaps 11;

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QY 1 EGDYSLCOOREK---LDDMKREMFTELHNGYRAAFARNYKT-SKMTMYVDTLEKAYK 56
DB 43 DGEWMTAKORGRFATTDNDMSLIL-DLHNKLR---SQVYPMASMEYMWVDELEERSAES 98
QY 57 SAEKCSSE--PSSEENYDVFSATATNIDPLEAG-----NSWMEGI-----94
DB 99 MAESCIMEHGPPAS-----LLPSIGNLGAHNGRYPPTFVQSGWDEVDSEYPIHEHC 152
QY 95 -----FELRGKYNNKNGKTSNINAMWDSHDKLCAVYDCS-----KTHVYCOY 139
DB 153 NPYCPRCSGPV-----CTHYQYVWATSNIGCAIHLCHNNIMIQWQIMPKAVYLVQNY 205
QY 140 GPEAKGDGKTYIEGAPCSRC-SPYGAG 166
DB 207 SPFGNMWGHAPYKKGRCPSACPPSPFGG 234

RESULT 24
ID 09UB03 PRELIMINARY: PRT: 220 AA.
AC 09UB03:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Vespid allergen antigen homolog.
GN VAH.
OS Mucheretia bancrofti.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidae;
OC Onchocercidae; Mucheretia.
OX NCBI_TaxID=6293;
RN (1)
RP SEQUENCE FROM N.A.
RA Sellman A.K., Steel C.S., Ottesen E.A., Nutman T.B.;
RT Identification of potentially protective antigens in human lymphatic
RT filariasis.
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DB EMBL: AF128091; AAD28256.1;
DR HSSP; P04284; ICFE.
DR InterPro; IPR001283; Allrgn_V5/TpX1.
DR Pfam; PF00188; SCP. 1.
DR PRINTS; PR00837; V5TFPLIKE.
DR PRODOM; PD000542; Allrgn_V5/TpX1; 1.
DR SMART; SM00198; SCP. 1.
SQ SEQUENCE 220 AA; 24617 MW; 7439F5DB1C96E978 CRC64;

Query Match 15.7%; Score 157; DB 5; Length 220;
Best Local Similarity 27.2%; Pred. No. 8, 2e-07;
Matches 50; Conservative 26; Mismatches 74; Indels 34; Gaps 10;

QY 12 KLDDDMREMFTELHNGYRAAFARNY-----KTSKMTMYVDTLEKAYKSAK 61
DB 23 QLTPOQRKDIYRONNKRPSLIRGKLKNNNGTYMPRGKNNMLQITWSCOLENSAORMNOC 82
QY 62 --SEEPSSEE---ENDYVF--SAATLNI-----PLEAGNSWSEIFELRGKYNNKNGKTS 109
DB 83 VFGHSPRNOGIGENYVWSSAVENTLRKTACTENGKSWSELPPLY-KHNSNNLTD 141
QY 110 NTA-----NMWDSHDKLCAV-VDC-SGKTHV-VCQYGPBAGKDGKTYIEGAPCS 158
DB 142 DVSROGVLFHTOMAGKTHKIGCGIATNCDSGRITLITICHSPAGNITLKNLYELGEPC 201
QY 159 RQSD 162
DB 202 KDGD 205

RESULT 25
ID 097149 PRELIMINARY: PRT: 220 AA.
AC 097149:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

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DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Vespid allergen antigen homolog.
GN VAH.
OS Mucheretia bancrofti.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidae;
OC Onchocercidae; Mucheretia.
OX NCBI_TaxID=6293;
RN (1)
RP SEQUENCE FROM N.A.
RA Hopkins R.M., McCarthy J.S.;
RT Cloning of the Mucheretia bancrofti venom allergen homolog.
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DB EMBL: AF109794; AAD16985.1;
DR HSSP; P04284; ICFE.
DR InterPro; IPR001283; Allrgn_V5/TpX1.
DR Pfam; PF00188; SCP. 1.
DR PRINTS; PR00837; V5TFPLIKE.
DR PRODOM; PD000542; Allrgn_V5/TpX1; 1.
DR SMART; SM00198; SCP. 1.
SQ SEQUENCE 220 AA; 24640 MW; 84314558E31540D4 CRC64;

Query Match 15.6%; Score 156; DB 5; Length 220;
Best Local Similarity 27.2%; Pred. No. 1e-06;
Matches 50; Conservative 26; Mismatches 74; Indels 34; Gaps 10;

QY 12 KLDDDMREMFTELHNGYRAAFARNY-----KTSKMTMYVDTLEKAYKSAK 61
DB 23 QLTPOQRKDIYRONNKRPSLIRGKLKNNNGTYMPRGKNNMLQITWSCOLENSAORMNOC 82
QY 62 --SEEPSSEE---ENDYVF--SAATLNI-----PLEAGNSWSEIFELRGKYNNKNGKTS 109
DB 83 VFGHSPRNOGIGENYVWSSAVENTLRKTACTENGKSWSELPPLY-KHNSNNLTD 141
QY 110 NTA-----NMWDSHDKLCAV-VDC-SGKTHV-VCQYGPBAGKDGKTYIEGAPCS 158
DB 142 DVSROGVLFHTOMAGKTHKIGCGIATNCDSGRITLITICHSPAGNITLKNLYELGEPC 201
QY 159 RQSD 162
DB 202 KDGD 205

RESULT 26
ID 020608 PRELIMINARY: PRT: 207 AA.
AC 020608:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE F99E11.9 protein.
GN F99E11.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Felodertinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN (1)
RP SEQUENCE FROM N.A.
RA Baynes C.;
RT Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RL [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=90069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 283:2012-2018(1998).
DB EMBL: Z70308; CAA94348.1;
DR InterPro; IPR001283; Allrgn_V5/TpX1.
DR Pfam; PF00188; SCP. 1.
DR PRINTS; PR00837; V5TFPLIKE.
DR PRODOM; PD000542; Allrgn_V5/TpX1; 1.
DR SMART; SM00198; SCP. 1.
SQ SEQUENCE 207 AA; 21932 MW; 5D6F6E96794B4C1A CRC64;

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Query Match      15.5%; Score 154.5; DB 5; Length 207;
Best Local Similarity 26.6%; Pred. No. 1.3e-06;
Matches 49; Conservative 19; Mismatches 71; Indels 45; Gaps 7;

OY 23 ELHNGYRAAFARNTKSK-----MRTWYDCTLEEKAYSAKCESEPSSE---70
DB 26 DANNKTRSAIAKSTYKAGTKRKEPATDMKRMKVVSTVAASNOYAWTC---PTGHSKGTG 82
OY 71 -----NVDYFSAATLNIPLLEAGNSWSEIFELRGKYRK-----NGKTSNIAM 114
DB 83 YGENTYWSMTSADYGSIDSYG---ETAAAMWKEKFODEGKMSNAMDITLFNSGIGHATQM 139
OY 115 VWDSDHDKLCAVAVDCS-----GRTHYVCCYGPPEAKGDKITTEGAPCSGSDGAG 166
DB 140 AANAATSSIGCGVKNKCGDASMRMNRKIAVCCYSPGNTGRIPTYKEGTTCSSCS---GS 196
OY 167 VTCD 170
DB 197 TKCD 200

RESULT 27
OY 093747 PRELIMINARY; PRT; 213 AA.
AC 093747;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE F49E11.4 protein.
GN F49E11.4
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Telodermidae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN 111
RP SEQUENCE FROM N.A.
RA Baynes C.;
RT Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
RX MEDLINE=99069613; PubMed=9851916;
RZ SEQUENCE FROM N.A.
RT "Genome sequence of the nematode C. elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
EMBL; 270308; CA94349.1;
DR InterPro; IPR001283; Allrgn_V5/Tpx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; VSTPLIKE.
DR PRODOM; PD000542; Allrgn_V5/Tpx1. 1.
DR SMART; SM00198; SCP; 1.
SQ SEQUENCE 213 AA; 23979 MW; ADD56E2B33A9D8A CRC64;

Query Match      15.3%; Score 153; DB 5; Length 213;
Best Local Similarity 27.1%; Pred. No. 1.8e-06;
Matches 45; Conservative 29; Mismatches 64; Indels 28; Gaps 7;

OY 24 LHNHYRAAR-----RMYKSKKRTVNDCTLEEKAYSAKCESEPS---SEEN 71
DB 31 VHNFSQALQQLSFRGVKPKPSASMRKISMKLTNAATKRFETCPKXHSVYVANTGES 90
OY 72 VDVFSAAATNIPLE---AGNSWSEIFELRG---KYVKNKGTSNIAN---MYWDSHK 121
DB 91 IFMHFSSISSTPEQATLAPQKMWNE-FETNGDSILYVHNSORFOIGHAVQMAHTTSK 149
OY 122 LGCAVAVDCSGKTH-----VVCQYGPPEAKGDKITTEGAPCSGSD 162
DB 150 VGGGYSKCAVGTPEQTWVVCYRYPQKNGINEGEPIYNEGETCTKPE 195

RESULT 28
OY 020609 PRELIMINARY; PRT; 212 AA.
AC 020609;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE F49E11.5 protein.
GN F49E11.5
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Telodermidae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN 111
RP SEQUENCE FROM N.A.
RA Baynes C.;
RT Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
RX MEDLINE=99069613; PubMed=9851916;
RZ SEQUENCE FROM N.A.
RT "Genome sequence of the nematode C. elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
EMBL; 270308; CA94349.1;
DR InterPro; IPR001283; Allrgn_V5/Tpx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; VSTPLIKE.
DR PRODOM; PD000542; Allrgn_V5/Tpx1. 1.
DR SMART; SM00198; SCP; 1.
SQ SEQUENCE 212 AA; 23359 MW; 5A4DB40539CB708C CRC64;

Query Match      15.2%; Score 152; DB 5; Length 212;
Best Local Similarity 24.5%; Pred. No. 2.3e-06;
Matches 51; Conservative 25; Mismatches 92; Indels 40; Gaps 8;

OY 4 YSLCOOREKLDDMEKMTLEHNGYRAAR-----RMYKSKKRTVNDCTLEEK 54
DB 13 FSCFETLCFSETGANTYLSNHLNSQILKRYVAGNSTPSPASNMKLIWDTLETETA 72
OY 55 YKSAKCESEPSSEEND-----VFSAAATLNIPLLEAGNSWSEIFELRGKYRK 104
DB 73 QDYSTCPTGHSASRANGENMYWMTSPVYTOTDAELLGNRSANLWSE-FOFG--WNG 129
OY 105 NGKTSNIAN-----MYWDSHKLCAVAVDCSGKTH-----VVCQYGPPEAKGDKIT 151
DB 130 NLTEELFNSGIGHATOMANATNKGICISKCSDSDFGTQYVVCYSPAGNYIGMDIY 189
OY 152 EEGAPCSGSDYGAAGVTCDDQWNLICI 179
DB 190 KSGETCSNCPD---GTNCES--STGLCV 212

RESULT 29
OY 016854 PRELIMINARY; PRT; 220 AA.
AC 016854;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Activation-associated secreted protein-1.
GN OV-ASP-1.
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_Taxid=6282;
RN 111
RP SEQUENCE FROM N.A.
RA STRAIN-FORREST;
RX MEDLINE=20416487; PubMed=10960168;
RA Tave W.; Pearlsman F.; Dmasech T.R.; Lustigman S.;
RT "Angiogenic activity of Onchocerca volvulus recombinant proteins
similar to vespid venom antigen 3."
RL Mol. Biochem. Parasitol. 109:91-99(2000).

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RP SEQUENCE FROM N.A.
RC STRAIN-FOREST.
RA Joseph G.T., Lustigman S.;
RT "Cloning and characterization of a cDNA clone, Ov B93 from a L3
RT library", (SEP-1999) to the EMBL/GenBank/DBJ databases.
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF020586; BAB69625.2; -.
DR HSSP: P04284.1; CFE.
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP: 1.
DR PRINTS: PR00837; V5TPX1KE.
DR ProDom: PD000542; Allrgn_V5/Tpx1; 1.
DR SMART: SM00198; SCP: 1.
DR PROSITE: PS01010; SCP_AGS_PRL_SCT_2; UNKNOWN_1.
SQ SEQUENCE 220 AA; 24510 MW; C089BFAE869EBAB CRC64;

Query Match 15.2%; Score 152; DB 5; Length 220;
Best Local Similarity 25.8%; Pred. No. 2,4e-06;
Matches 47; Conservative 24; Mismatches 69; Indels 42; Gaps 9;

OY 9 QREKLDMDREMFTEHNGYRAAFARNY--KTSKRTMYVDCITLBEKAYKSAEC--SEE 64
DB 28 EKKIKVQNNKYSDDLNGKLNKRGTYMPGKMLTETWCKLESQAQRANQICRHG 87
OY 65 PSSEENV--DVF-----SATLNIPLEAGSMWSEIFELRGVYKNGKTS 109
DB 88 PROQEGYGVNYAVYSVSEGLKKTGCT----DAKGSWSKL---PLYENNPSNN 138
OY 110 -----NIANNVWPSHDKLGCAV--VDCG--KTHVCOYGPBKAQDGKTYEBA 155
DB 139 MHWVAGGYLHFTQMANKRTKICGVANCGDGRLLVICHYPSGNMVGVIYHGRN 198
OY 156 FC 157
DB 199 FC 200

RESULT 30
OY 092006 PRELIMINARY; PRT; 188 AA.
AC 092006;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Late gestation lung protein 1.
GN LGI1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid:10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MISTAR; TISSUE-LUNG;
RX MEDLINE-99292450; PubMed-10362728;
RA Kaplan F., Ledoux P., Kaasamali F.Q., Gagnon S., Post M., Koehler D.,
RA Demling J., Swezey N.B.;
RT "A tumor developmentally regulated gene in lung mesenchyme: homology
RT to a novel developmentally regulated gene in lung mesenchyme: homology
RT to a novel developmentally regulated gene in lung mesenchyme: homology
RL Am. J. Physiol. 276:R1027-R1036(1999).
DR EMBL: AF109674; AAD16986.1; -.
DR HSSP: P04284.1; CFE.
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP: 1.
DR PRINTS: PR00837; V5TPX1KE.
DR ProDom: PD000542; Allrgn_V5/Tpx1; 1.
DR SMART: SM00198; SCP: 1.
DR PROSITE: PS01010; SCP_AGS_PRL_SCT_2; 1.
SQ SEQUENCE 188 AA; 21907 MW; 5B6C7715360BCE CRC64;

Query Match 14.8%; Score 148; DB 11; Length 188;
Best Local Similarity 26.9%; Pred. No. 4,6e-06;
Matches 52; Conservative 22; Mismatches 61; Indels 58; Gaps 11;

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OY 24 LHNGYRAAFARNY--KTSKRTMYVDCITLBEKAYKSAECSE--PSSEENVVPSATL 80
DB 2 LHKLR-----GVYTPASMETWDELEERSAAMQCNLMEHCPAS-----LLVSGO 52
OY 81 NITLENG-----NSWSEIFELRGVY-----KNGKSNIANMY 116
DB 53 NLAVHGRIRSPGFVOSWIDEV-----KDTYPIPEHCNPKPCSCGAMCTHTOMY 107
OY 117 DSHDKLGCAVYDC-----SGTHVCOYGPBKAQDGKTYEBAQPCRC--SDYGA 165
DB 108 ATNNKIGCAVHTCRSMYSWQDIWENAVYLWNTSPKGNWIGEAPYRHRGPCSECPSTYG 167
OY 166 GVTCDDDWQNLIC 178
DB 168 G--C-----RNNLC 174

RESULT 31
OY 044932 PRELIMINARY; PRT; 220 AA.
AC 044932;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Vespid allergen antigen homolog (Venom allergen antigen-like protein
DE 1).
OS Brugia malayi.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidae;
OC Onchocercidae; Brugia.
OX NCBI_Taxid:6279;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TBS LABS.
RA McCarthy J.S., Hopkins R.M.;
RT "Cloning of the Brugia malayi VA homolog";
RT Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA Murray J., Gregory W.F., Almadja A.K., Maizels R.M.;
RT "Expression and immune recognition of Brugia malayi VAL-1, a homolog
RT of Vespid venom allergens and Ancylostoma secreted proteins";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF042088; AAB97283.2; -.
DR EMBL: AF334661; AAK12274.1; -.
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP: 1.
DR PRINTS: PR00837; V5TPX1KE.
DR ProDom: PD000542; Allrgn_V5/Tpx1; 1.
DR SMART: SM00198; SCP: 1.
SQ SEQUENCE 220 AA; 24761 MW; F22F11AD7768FE65 CRC64;

Query Match 14.8%; Score 148; DB 5; Length 220;
Best Local Similarity 29.4%; Pred. No. 5,6e-06;
Matches 45; Conservative 20; Mismatches 48; Indels 40; Gaps 10;

OY 41 MRMVYDCITLBEKAYKSAEC--SEPSSEE-----ENTDV-----SATLNIP 83
DB 62 MLIKSCLENSAQRANOCYFCHSPRNRGICGENYAVWSEVEKLRNACT----- 117
OY 84 LEAGNSWSEIFELRGVYK--NGKTSNIA-----NMYDSHDKLGCAV--VDC-S 130
DB 118 -EAGKSMSEL-----PKLYKONPSNNLTDVAKQCYLHFTQMANGKTHKIGCAIATDCG 172
OY 131 GKTHV--VCOYGPBKAQDGKTYEBAQPCRCSD 162
DB 173 GRTLIAICHYSPAGNMKLEIYELGECRTDSD 205

RESULT 32
OY 018543 PRELIMINARY; PRT; 208 AA.
AC 018543;
DT 01-NOV-1996 (TREMBLrel. 01, Created)

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DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE C39E9.2 Protein.
GN C39E9.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP Sams M.A.;
RA Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; Z70307; CA9435.1; -.
DR HSSP; P04284; ICPE.
DR InterPro; IPR001283; Allrgn_V5/Tpxl.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPXLR.
DR ProDom; PD000542; Allrgn_V5/Tpxl; 1.
DR SMART; SM00198; SCP; 1.
SQ SEQUENCE 208 AA; 21928 MW; 3DAFBCB60CC0E5 CRC64;

Query Match 14.7%; Score 146.5; DB 5; Length 208;
Best Local Similarity 24.3%; Pred. No. 7.2e-06;
Matches 45; Conservative 26; Mismatches 63; Indels 51; Gaps 7;

QY 24 LINGRAFAFANYTSK-----MRTWYDCTLEEKAYKSAKESSE----- 64
DB 30 VHTLRSLRAGTYVAATLPIEAGNSMWSEIFELRGVYNNKNGKTSNIAN----- 113
QY 65 -----PSESEENVDFSAATLPIEAGNSMWSEIFELRGVYNNKNGKTSNIAN----- 113
DB 90 LVMYTSNTYINIDQFA-----TGSAAKEFQDYG--WSSNTLSMLFTNGIGHA 139
QY 114 --WVWDSHDKGCAVVDSCS-----GKTHVVCQYGPAPKADGKTIYEGAPCSRCSDYGA 165
DB 140 TQMAAKNTNLGCGVKNCGKDTNGFNKVTYVVCQYKPOGNYLNONITSTGSCSKP---S 196
QY 166 GVTCD 170
DB 197 GTSCE 201

RESULT 33
Q9N313 PRELIMINARY; PRT; 246 AA.
ID Q9N313;
AC Q9N313;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 26.9 kDa protein.
GN Y51H7C.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;

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RA Bradshaw-Cordum H.; Dubugue T.;
RT "The sequence of C. elegans cosmid Y51H7C."
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RX Waterston R.;
RT "Direct Submission."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC024805; AA83935.1; -.
DR InterPro; IPR001283; Allrgn_V5/Tpxl.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPXLR.
DR ProDom; PD000542; Allrgn_V5/Tpxl; 1.
DR SMART; SM00198; SCP; 1.
KM Hypothetical protein.
SQ SEQUENCE 246 AA; 26913 MW; BID7D59DC07B399 CRC64;

Query Match 14.4%; Score 143.5; DB 5; Length 246;
Best Local Similarity 24.5%; Pred. No. 1.7e-05;
Matches 45; Conservative 24; Mismatches 68; Indels 47; Gaps 6;

QY 23 ELHNGRAFAFANYTSK-----MRTWYDCTLEEKAYKSAKESSEPSSEENV 73
DB 29 DAHNEFRSSIAKGTYYTGILHAPATINIMKKNVTIATAQNNANNCPRGHGPLEGVS 88
QY 74 -----VFSATLPIEAGNSMWSEIFELRGVYNNKNGKTSNIAN----- 113
DB 89 GECMSGHINASGVNHLGAVAAKANSSE-----YTKKGWETDVMSDEPFNSGVGA 140
QY 114 --WVWDSHDKGCAVVDSCGK-----THVVCQYGPAPKADGKTIYEGAPCSRCSDYGA 166
DB 141 IIMTWYQVYVGGVYKLCQKEDYQYLAIVYCKYWGQNGKINYESGPTCSACP--PN 197
QY 167 VTCD 170
DB 198 TTCD 201

RESULT 34
Q93746 PRELIMINARY; PRT; 207 AA.
ID Q93746;
AC Q93746;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE F49E11.6 protein.
GN F49E11.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Baynes C.;
RA Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; Z70308; CA94350.1; -.
DR HSSP; P04284; ICPE.
DR InterPro; IPR001283; Allrgn_V5/Tpxl.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPXLR.
DR ProDom; PD000542; Allrgn_V5/Tpxl; 1.
DR SMART; SM00198; SCP; 1.
SQ SEQUENCE 207 AA; 22006 MW; 3072C43F25FEE626 CRC64;

Query Match 14.3%; Score 143; DB 5; Length 207;

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SEQUENCE FROM N.A.
RC STRAIN-BRISTOL NZ;
RA Waterston R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC006655; AAF39874.1;
DR InterPro: IPR001283; Allrgn_V5/TPx1.
DR Pfam: PF00188; SCP: 1.
DR PRINTS: PR00837; V5TPX1KE.
DR PRODOM: PD000542; Allrgn_V5/TPx1; 1.
DR SMART: SM00198; SCP: 1.
SQ SEQUENCE 208 AA; 22470 MW; 917E04AD6C1DBF33 CRC64;

Query Match 14.1%; Score 141; DB 5; Length 208;
Best Local Similarity 24.0%; Pred. No. 2.4e-05;
Matches 43; Conservative 28; Mismatches 70; Indels 38; Gaps 8;

OY 25 HNGYRADA-RNY-----KTSKRTMYDCTLEERKAYSAKSCSEEPSEENVDF 75
DB 30 HNDLSAATAGNYDACTLEPPAANKIKWDSTVASSAQYANTCPDHSCTGTEGENLY 89
OY 76 SAATINIP-----LEAGNSW-----WSEIFELRGKVTYNNKNGKTSNINAWYDSD 120
DB 90 WSMSSAATPTSDKFGVAASNSWEKEFODYGEWSTY-HDADLPDSG--IGHATOMAAETN 146
OY 121 KLGCAVYDCSG-----KTHVCCYGPPEAKGDKGKTYIEGAPGSCSDYAGYTCDD 171
DB 147 KTGCGVKNCKGKDSNNMNTAVAYACYDQAGNMDSDIYSGDTCSFC--SGSKCE 202

RESULT 38
OY 018347 PRELIMINARY; PRT; 221 AA.
AC 018347;
DR 01-JAN-1998 (TEMBREL) 05, Created
DR 01-JAN-1998 (TEMBREL) 05, Last sequence update
DR 01-JUN-2002 (TEMBREL) 21, Last annotation update
DE Venom allergen antigen 5-like protein.
GN NDIVAB33.
OS Dirofilaria immitis (Canine heartworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spluridae; Filarioidae;
OC Onchocercidae; Dirofilaria.
OX NCBI_TextID=6287;
RN [1]
RP SEQUENCE FROM N.A.
RA Tripp C.A., Wisniewski N.;
RT "Dirofilaria immitis larval cDNA clone isolated with immune dog sera."
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF001100; AAB62535.1;
DR InterPro: IPR001283; Allrgn_V5/TPx1.
DR Pfam: PF00188; SCP: 1.
DR PRINTS: PR00837; V5TPX1KE.
DR PRODOM: PD000542; Allrgn_V5/TPx1; 1.
DR SMART: SM00198; SCP: 1.
DR PROSITE: PS01010; SCP_AGS_PRL_SCT_2; UNKNOWN.1.
SQ SEQUENCE 221 AA; 25158 MW; 5542BA4B455046F7 CRC64;

Query Match 14.1%; Score 141; DB 5; Length 221;
Best Local Similarity 27.0%; Pred. No. 2.5e-05;
Matches 57; Conservative 17; Mismatches 65; Indels 72; Gaps 12;

OY 7 COOREKLDMDREMTLHNGYRAAFARNY-----KTSKRTMYDCTLEERKAYK 56
DB 19 CEGKGLTPTERKNITQT-KNYSRLIRKGLKNDGYLMPGKMLMMDCKLEKSAON 77
OY 57 SAKC---SEEPSE---ENVDF-----SAATINIPLEAGNSWSEIFELRG 99
DB 78 WANNCYFGHSPSSERIGENVYAYSSGVLDLKKTAGT---DAGRLMSEL---E 128
OY 100 KYVN---KNGKTSNIA-----NNYWDSDHKLCAVYDCSGKTR-----VYCO 138
DB 129 KYSDNPSNNLTSSEVAMENILHFTQVAMGETYKLG-----SGVDHNIYVAVATLWIFCH 182

OY 139 YGPEAKDGKTYIEGAPC-----SRCS 161
DB 183 YFPGNMVYDLIELGPNCKHNKDCRTRCS 213

RESULT 39
OY 018549 PRELIMINARY; PRT; 211 AA.
AC 018549; Q20610;
DR 01-NOV-1996 (TEMBREL) 01, Created
DR 01-NOV-1998 (TEMBREL) 08, Last sequence update
DR 01-JUN-2002 (TEMBREL) 21, Last annotation update
DE F49E11.11 protein.
GN F49E11.11
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditoidae;
OC Rhabditidae; Rhabditinae; Caenorhabditis.
OX NCBI_TextID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Baynes C.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RE SEQUENCE FROM N.A.
RA MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnecough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper A.,
RA Gratton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten N., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smaildon N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
RA Thierzy-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Woldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans."
RL Nature 368:32-38 (1994).
RN [3]
RP SEQUENCE FROM N.A.
RA Sims M.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z70308; CA94354.1;
DR EMBL: Z70307; CA94354.1; JOINED.
DR EMBL: Z70307; CA94354.1;
DR EMBL: Z70308; CA94354.1; JOINED.
DR HSSP: P04284; ICPE.
DR InterPro: IPR001283; Allrgn_V5/TPx1.
DR Pfam: PF00188; SCP: 1.
DR PRINTS: PR00837; V5TPX1KE.
DR PRODOM: PD000542; Allrgn_V5/TPx1; 1.
DR SMART: SM00198; SCP: 1.
DR PROSITE: PS01010; SCP_AGS_PRL_SCT_2; UNKNOWN.1.
SQ SEQUENCE 211 AA; 22676 MW; ADF90C8E263F58F2 CRC64;

Query Match 14.1%; Score 140.5; DB 5; Length 211;
Best Local Similarity 24.0%; Pred. No. 2.7e-05;
Matches 47; Conservative 25; Mismatches 71; Indels 53; Gaps 8;

OY 15 DDMREMTLHNGYRAAFARNYKTSKMT-----WYDCTLEERKAYSAKSCSEEP 65
DB 22 ESTQOFTYDHLNKLRTSIAKGYVAKGTTRAGSNLKKMKWPTLATATPOTFANTCRGH 81
OY 66 SEE---EN-----VDVSAATINIPLEAGNSWSEIFELRGKVTYNNKNGKTSN 110
DB 82 SNAACVGENLYKRWSSLPFSGMDITGG-----AAVSAMQDEEQYQ--WTNNFTQA 131
OY 111 IAN-----WYWDSDHKLCAVYDCSGKTR-----GKTHVCCYGPPEAKGDKGKTYIEG 154
DB 132 LNTGIGHATOMAAETNIGLGCYVANKGCPPELNNINRAVAYACYDQAGNMDSDIYSG 191
OY 155 APCSRCSDYAGYTCDD 170

DB 192 TTCACP---TGTTC 204

RESULT 40

09C035 PRELIMINARY; PRT: 332 AA.

AC 09C035 01-JUN-2001 (TREMBlrel. 17, Created)

DF 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

GN 492150801IRK protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=TESTIS;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawaji J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Glass C., King B., Kochwa H.,

RA Schiri L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monoberts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez S., Sakamoto N.,

RA Nozaki H., Sato K., Schenbach K., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Watanabe-Borls A., Yoshida K., Hasegawa I., Kawaji H., Kohsaki S.,

RA Hayashizaki Y.,

RT Functional annotation of a full-length mouse cDNA collection.

RL Nature 409:685-690(2001).

DR EMBL: AK015834; BAB29594.1; -

DR HSSP: P04284; ICFE.

DR MGD: MGI:1914787; 492150801IRK.

DR InterPro: IPR001283; Allrgn_V5/Tpx1.

DR Pfam: PF00188; SCP: 1.

DR PRINTS: PR00837; V5TPXLIKE.

DR PRODOM: PD000542; Allrgn_V5/Tpx1; 1.

DR SMART: SM00198; SCP: 1.

SQ SEQUENCE 332 AA; 37784 MW; CEBDBA2A0697FDDC CRC64;

Query Match 14.1%; Score 140.5; DB 11; Length 332;

Best Local Similarity 29.1%; Pred. No. 4.7e-05;

Matches 55; Conservative 20; Mismatches 67; Indels 47; Gaps 12;

OY 14 DDDREFFTELHNGYR-AAFAANRYKTSKMTWYDCTLEEKAYSAEKSEEPSSE----- 68

DB 47 DVDFINXYVGLHNEHGLGVFPVGV---NLRFPMWDVALSRTFAAGKCKMYSNHTLIDLK 103

OY 69 EENDVFSATLNI---PLE-----AGNSWSEIFELNGKYNN-----KNGKTSNIA 112

DB 104 HESHPVTEIGENMMWGPVEDEFTVTAIRSMHE-----RKSYSYINDTCVEQONSHIT 158

OY 113 NMWDSHDKIGCAVYVNC---GKTHV---VCOYGPBAKDKGTI---YEGAPRCSCSD 162

DB 159 OLWVDSYKYGCAVYSCAAGFTHALFTICATP-----GGLTRRYQAGQPCSRC--- 211

OY 163 YGAGVTCDD 171

DB 212 -GPDQCTD 219

RESULT 41

09D2R3

AC 09D2R3 PRELIMINARY; PRT: 434 AA.

DF 01-JUN-2001 (TREMBlrel. 17, Created)

DE 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

GN 1810049K24R1K protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=PANCREAS;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawaji J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Glass C., King B., Kochwa H.,

RA Schiri L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monoberts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez S., Sakamoto N.,

RA Nozaki H., Sato K., Schenbach K., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Watanabe-Borls A., Yoshida K., Hasegawa I., Kawaji H., Kohsaki S.,

RA Hayashizaki Y.,

RT Functional annotation of a full-length mouse cDNA collection.

RL Nature 409:685-690(2001).

DR EMBL: AK019034; BAB31519.1; -

DR HSSP: P04284; ICFE.

DR MGD: MGI:1926142; 1810049K24R1K.

DR InterPro: IPR001283; Allrgn_V5/Tpx1.

DR Pfam: PF00188; SCP: 1.

DR PRINTS: PR00837; V5TPXLIKE.

DR PRODOM: PD000542; Allrgn_V5/Tpx1; 1.

DR SMART: SM00198; SCP: 1.

DR PROSITE: PS01010; SCP_AGS_PRL-SC7_2; 1.

SQ SEQUENCE 434 AA; 48593 MW; CZ5067EB14647AC0 CRC64;

Query Match 14.0%; Score 140; DB 11; Length 434;

Best Local Similarity 25.8%; Pred. No. 7.2e-05;

Matches 48; Conservative 21; Mismatches 73; Indels 44; Gaps 8;

OY 24 LHHNGRAFAFARNY-KTSKMTWYDCTLEEKAYSAEKSEEPSSEENDVFSATLNI 82

DB 2 LHHKLR---GVYPPASNMHEHWDELEERSAAMAHRLIMEHGP---AGILRSIGONTL 54

OY 83 PLEAG-----NSWSEIFEL-----RGKYNNKNGKTSNIAANWVDSHDKLG 123

DB 55 AVHWGRYRSPGFHVQSYDEVKDYTYPRPHCTPRCHRECRSGPMCTHYTQWVWATTKIG 114

OY 124 CAVVCC-----SGKTHVCOYGPBAKDKGTIYEGGACGSC--SDGAGVTCDD 172

DB 115 CAVHCRMANWMDPTWENAVYLVCNTPSPKMWIGEARIKNGRCSCSCSGGCL----- 170

OY 173 WNTLC 178

DB 171 ---NLC 174

RESULT 42

022421 PRELIMINARY; PRT: 262 AA.

AC 022421 022421

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DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE T12A7.3 protein.
GN T12A7.3
OC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Kennard N.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE-99069613; PubMed-9851916;
RX none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; 273911; CA98140.1; -.
DR InterPro; IPR001283; Allrgn_V5/TPx1.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00188; SCP; 1.
DR ProDom; PD000542; Allrgn_V5/TPx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN; 1.
SQ SEQUENCE 262 AA; 29919 MW; 1B51A10F5F603ABA CRC64;

Query Match 13.9%; Score 139; DB 5; Length 262;
Best Local Similarity 26.2%; Pred. No. 48e-05;
Matches 59; Conservative 20; Mismatches 66; Indels 80; Gaps 11.

OY 14 DDDREMEFTE-----LHNGY-----RAAFARNYKT-----SKMTMYDCTL 50
DB 59 DDEDEHEFMENEAFCDDNYCANNYPGSQLAG-NFYAKRTKRAAGSNKKFYNNAL 117
OY 51 EEKAYKAEKSEPESEENVDFAATLNTPLKNGSNW-----S 92
DB 118 ERSKYSNOK--NPSQHS-----FTDIGNLFWHSTRREDNRKKGPMALIS 163
OY 93 EIFELKRYTKKNGKTSNI-----ANNWDSHDKLCQAVDCS-----GKTH 134
DB 164 WIKFERKFWDSNLTNDLFGSGVGHATQWMDTYQMCVASHKEIKRTGRPTTKIC 223
OY 135 VVCOYGPEAKGDKITYEGAPCSGSDYAGVTCDDDMQNLICI 179
DB 224 VVCHYWKGNLYNEPIYLEGPPCSKCE---SKKCDK--RTGLCI 262

RESULT 43
O18539 PRELIMINARY; PRT; 209 AA.
AC 018539;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-JAN-1998 (Tremblrel. 05, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE C39E9.5 protein.
GN C39E9.5
OC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Sims M.A.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE-99069613; PubMed-9851916;
RX none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."

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RL Science 282:2012-2018(1998).
DR EMBL; 270307; CA94331.1; -.
DR HSSP; P04284; 1CFE.
DR InterPro; IPR001283; Allrgn_V5/TPx1.
DR Pfam; PR00188; SCP; 1.
DR PRINTS; PR00837; V5TPXLIKE.
DR ProDom; PD000542; Allrgn_V5/TPx1; 1.
DR SMART; SM00198; SCP; 1.
SQ SEQUENCE 209 AA; 22319 MW; 50504B53A1DA67 CRC64;

Query Match 13.9%; Score 138.5; DB 5; Length 209;
Best Local Similarity 24.7%; Pred. No. 4e-05;
Matches 46; Conservative 30; Mismatches 71; Indels 39; Gaps 7;

OY 18 REMFTLNGYRAAFARNYKSK-----MRTVYDCTLEEKAYSAEKSEPPSE 68
DB 23 KQMVNHNAAVRSIAAGEVYAKGTRKDSATNMKMDSLAQSNVYANCPCMQHSPD 82
OY 69 EENVDFSAATLNTPL-----EAGNSWSEIFELRGKYNNKNGKTSNIAN----- 113
DB 83 KSYGENTLFWAYSSPITDLDKRYQSAVDTVWSE-FQWFG--WNSNKEFTALMNTGIGHAT 139
OY 114 -MYWDSHDKLCQAVDC-----SGTHVVCQYGPEAKGDKITYEGAPCSGSDYG 164
DB 140 OVAMSAFGQVCGAKNGCADSVAGSYKATVCOYKPGNYLFKNINYSAGKACSCAP--- 196
OY 165 AGVTCO 170
DB 197 AGTSC 202

RESULT 44
O18538 PRELIMINARY; PRT; 209 AA.
AC 018538;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-JAN-1998 (Tremblrel. 05, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE C39E9.4 protein.
GN C39E9.4
OC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Sims M.A.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE-99069613; PubMed-9851916;
RX none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; 270307; CA94330.1; -.
DR HSSP; P04284; 1CFE.
DR InterPro; IPR001283; Allrgn_V5/TPx1.
DR Pfam; PR00188; SCP; 1.
DR PRINTS; PR00837; V5TPXLIKE.
DR ProDom; PD000542; Allrgn_V5/TPx1; 1.
DR SMART; SM00198; SCP; 1.
SQ SEQUENCE 209 AA; 22459 MW; D9A915316027AFNA CRC64;

Query Match 13.8%; Score 137.5; DB 5; Length 209;
Best Local Similarity 24.3%; Pred. No. 5e-05;
Matches 46; Conservative 21; Mismatches 75; Indels 47; Gaps 7;

OY 18 REMFTLNGYRAAFARNYKT-----SKMTMYDCTLEEKAYSAEKS----- 62
DB 25 QQFIYDLNHSFRSLATAGTYSINGTLKPAGSNIRKMSDSTLATSQTYANTCPTGFSNT 84
OY 63 -----EPPSSEENVDFSAATLNTPLKAGNSWSEIFELRGKYNNKNGK----- 107

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